protein search, using sw model

OM protein

Run on:

GenCore Copyright (c) 1993

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

908470 seqs, 133250620 residues

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Scoring table:

Title: Perfect score:

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Streptococcus poly
Streptococcus poly
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Lactococcus lactis
Novel human direction
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Seven-pass transme
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Novel
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                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babèsia microti BMNI-16 antigen sequence.
                                                                                                                             AAU07053
ABP29648
ABP30060
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW27161
AAU68533
AAU02196
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AAM50866
AAU74826
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AAU16043
AAM93742
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ABB63417
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AAO04655
ABP29775
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ABP27080
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ABG24086
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ABG01527
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                                               AAU19897
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96US-0723142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV22746.
Babesia microti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-APR-1997;
01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton R,
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Babesia microti an
B. microti BNNI-17
Babesia microti an
Babesia microti an
B. microti BNNI-17
Babesia microti an
Arabidopsis thalia
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Babesia microti BM
                                                                                                                             (without alignments)
476.010 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_101002:*

| SIDSS/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT:*
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            version 5.1.6 - 2003 Compugen Ltd.
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102
1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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SUMMARIES

DB

Query Match Length

Score

Result ્ટ AAY24357 AAB30206 ABB88951 AAG34732 AAG28927

AAY24353 AAB30202 AAW56296

ABB88948

13 22 23 23 23 23 23 23 23

245 245 245 245 32 32 32 32 150 195

73.5 73.5 73.5 73.5 70.6 35.3 35.3

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antibodies to detect the corresponding antigen. It is also
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                                                                                     245 AA;
                                                                                                                                                                                                                                                                                                                                                                                  Babesia microti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bruinsma E,
Sleath PR;
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                                                                                      Seguence
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                                                                                                                                                                                                                                                                       Gaps
                                                                   one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection by detecting specific antibodies in usual immunoassays. Infection was also diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
 transformed cells and antibodies, useful for diagnosis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                                                                                                                Length 245;
                                                             a polypeptide comprising at least
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                              DB 19;
7.4e-08;
                                                                                                                                                                                                                                                                                                            1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia microti BMNI-17 antigen sequence.
                                                                                                                                                                                                                                              Score 75;
Pred. No. 7
            infection and in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection and in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 67-68; 113pp; English
                                  Claim 1; Page 66; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sg,
                                                                                                                                                                                                                                                                                                                                                                                 AAW56297 standard; Protein; 245
                                                                                                                                                                                                                                              73.5%;
53.1%;
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96US-0723142.
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                                                                                                                                                                                                                                                        Local Similarity 53.1
hes 17; Conservative
                                                             The sequence is that of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R, Lodes MJ,
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N-PSDB; AAV22747.
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                                                                                                                                                                                                                       245 AA;
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01-0CT-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                            have similar symptoms but require different treatments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed
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                                                                                                                                                                                                                Score 75; DB 19;
Pred. No. 7.4e-08;
0; Mismatches 15
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Pred. No. 7.4e-08;
                                                                                                                                                                                                                                                                                                                                                          1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated Babesia microti polypeptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 84; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY24353 standard; Protein; 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babesia microti antigen BMNI-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                          Query Match
Best Local Similarity 53.1
Matches 17; Conservative
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Les 17; Conservative
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RESULT

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The present invention relates to novel Babesia microti antigens and the coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesia microti; antigen; immunogen; diagnosis; infection; vaccine; immunity; detection.
                                                                                                                                                                                                                                                                                                         New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                      Sleath PR, McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3abesia microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 75; DB 23;
Pred. No. 7.4e-08;
0; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                        Lodes MJ, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                               Claim 13; Page 87; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY24357 standard; peptide; 32 AA.
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illarity 53.1%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Met,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= Pro,
                                                             27-JUN-2000; 2000US-0605724.
07-SEP-2000; 2000US-0656688.
10-0CT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0737178.
26-FEB-2001; 2001US-0794764.
              09-MAY-2001; 2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1999 (first entry)
                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                          WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Aisc-difference 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 AA;
                                                                                                                                                                                                                                                                          N-PSDB; ABL89338
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                                                10-MAY-2000;
                                                                                                                                                                                                                        Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY24357;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                      Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 75; DB 21; Length 24
Pred. No. 7.4e-08;
0; Mismatches 15; Indels
                                                                                                                                                                    parasite; tick-borne illness; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                   B. microti BMNI-17 antigen SEQ ID NO: 32.
                                                                                                                                                                                      disease prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 81-82; 118pp; English.
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                            AAB30202 standard; Protein; 245 AA.
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Best Local Similarity 53.1%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-US09136
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17-MAR-2000; 2000US-0528784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed SG, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-686939/67
                                                                                                                                                                    Babesiosis; rodent
                                                                                                                                                                                      disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 AA;
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                                                               AAB30202;
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RESULT 5 ABB88948

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Gaps

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Indels

Length 245;

and their

Homer MJ;

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from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                          New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
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                                                                                                                                                                      McNeill PD;
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4.1e-08;
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                                                                                                                                                                        Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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                                                                                                                                                                      Houghton RL,
                                                                                                                                                                                                                                                                                                                              Claim 6; Page 85; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= Met, Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB88951 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Tyr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Leu,
                                               05-APR-2000; 2000WO-US09136
                                                                              05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
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                                                                                                                                                                                                         WPI; 2000-686939/67.
                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                          Lodes MJ,
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Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 AA;
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            12-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                        Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B.microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes isolated polypeptides comprising cific immunogenic portions of Babesia microti. AAX88993 to AAX88994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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. 4.1e-08;
ches 0;
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Pred. No. 4.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lodes MJ,
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/label= Ile, Phe
21
                                             Val
                                                                                                                                                      Leu
                                                                                                                                                                                                                         label= Thr, Ile
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100.0%; Pre
                                                                                                                                                                                                                                                          /label= Cys, Tyr
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                                                                                                                   label= Met,
                                                                                                                                                                                       label= Val,
                                             label- Ala,
                                                                                label= Leu,
                                                                                                                                                      label- Ser,
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Best Local Similarity 100.
Matches 32; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CORI-) CORIXA CORP.
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disease diagnosis;
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                             Misc-difference
                                                            Misc-difference
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Sequence

/label= Leu, Pro

Val

'label- Ala,

label= Ile,

Misc-difference Misc-difference

Babesia microti WO200060090-A1

AAB30206;

RESULT 7

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99US-0130891.
99US-0131449.
99US-0132048.
                            2000EP-0301439
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99US-0128714
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                            25-FEB-2000;
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 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                         Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing immune response against B. microti infections
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0
                                                                                                                                                                                                                                                                                                                                                        McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 70.6%; Score 72; DB 23; Length 32; Best Local Similarity 100.0%; Pred. No. 4.1e-08; Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 42309.
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                                                                                           'label- Thr, Ile
                                                                                                                      /label= Cys, Tyr
              /label= Met,
                                       'label= Ser,
                                                                label= Val,
                                                                                                                                                                                                                                          27-JUN-2000; 2000US-0605724.
07-SEP-2000; 2000US-0656688.
10-0CT-2000; 2000US-068436.
13-DEC-2000; 2000US-07317178.
26-FEB-2001; 2001US-0794764.
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                                                                                                                                                                                                                                2000US-0569098
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Misc-difference 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 AA;
                         Misc-difference
                                                    Misc-difference
                                                                             Misc-difference
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Secrist H;
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99US-0142803.
99US-0142920.
99US-0142977.
                                   99US-0143542.
99US-0143624.
99US-0144005.
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990S-0144086.
990S-0144325.
990S-0144331.
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990S-0145913.
990S-0145918.
990S-0145919.
990S-0146388.
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9905-0148319.
9905-0148341.
9905-0148565.
9905-01498684.
9905-0149368.
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99US-0154779.
99US-0155139.
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99US-0147260.
99US-0147303.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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43.8%; Pred. No. 7.7;
tive 2; Mismatches
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9908 - 0155659

9908 - 0156458

9908 - 0156458

9908 - 0157117

9908 - 0158029

9908 - 0158029

9908 - 0158029

9908 - 0159294

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Best Local Similarity 43.8
Matches 7; Conservative
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99US-0121825. 99US-0123180. 99US-0123548.

25-FEB-1999; 05-MAR-1999; 09-MAR-1999;

25-FEB-2000; 2000EP-0301439

06-SEP-2000

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990S-0144085. 990S-0144086. 990S-0144331. 990S-0144331. 990S-0144333. 990S-0144333. 990S-0144334. 990S-0144336. 990S-014436. 990S-0144884. 990S-0145086. 990S-0145086. 990S-0145089.	990S - 0145192. 990S - 0145145. 990S - 014524. 990S - 0145276. 990S - 0145913. 990S - 0145918. 990S - 0145919. 990S - 0145919. 990S - 0146386. 990S - 0146386. 990S - 0147304. 990S - 0147204. 990S - 0147204. 990S - 014720. 990S - 014720.	99US-0147935. 99US-0148171. 99US-0148341. 99US-0148845. 99US-0148684. 99US-0149368. 99US-0149722. 99US-0149722. 99US-0149722. 99US-0149723. 99US-0149902. 99US-0149902. 99US-0149930. 99US-015066. 99US-015066. 99US-0151065.	99US-0152363. 99US-0153070. 99US-0153078. 99US-0154018. 99US-0154039. 99US-0155139. 99US-0155486. 99US-0155659. 99US-015659. 99US-015659. 99US-015659.
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2000US-235484P.
2000US-235834P.
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2000US-218290P
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2000US-233063P
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20-OCT-2000;
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2000US-180628P.
2000US-184664P.
                                                         99US-0159293.
99US-0159294.
99US-0159295.
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99US-0159330.
99US-0159331.
99US-0159637.
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99US-0159584.
99US-0160741.
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2000US-205515P.
2000US-209467P.
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99US-0161404
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99US-0162142
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                                                                                                                                                                                                                                                           99US-01607
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Best Local Similarity 43.8
Matches 7; Conservative
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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25-0CT-1999;
25-0CT-1999;
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26-0CT-1999;
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19-MAY-2000;
07-JUN-2000;
                                 12-0cr-1999
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04-FEB-2000;
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28-OCT-1999
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Gaps
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                                                                                                                        Length 96;
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                                                                                                                    DB 22;
                                                                                                                Score 35; DB 2
Pred. No. 8;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      labour; menstrual cycle; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU18132 standard; Protein; 96 AA
                                                                                                            34.3%;
nilarity 54.5%;
Conservative 2
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                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                96 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200155201-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 - AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU18132;
                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides human cDNAs, proteins and related genomic DNAs. These can be used in the treatment of neural, immune system, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal and proliferative disorders and inflammation. The present sequence is a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecule encoding an inflammation-associated polypeptide is used in preventing, treating or ameliorating a medical condition .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11; SEQ ID NO: 659; 859pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
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N-PSDB; ABA06573.
20 - OCT - 2000;
20 - O
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
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17-NOV-2000;
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PR 05-SEP-2000; 2000US-0229509.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-021243.
PR 06-SEP-2000; 2000US-021144.
PR 08-SEP-2000; 2000US-021144.
PR 08-SEP-2000; 2000US-021144.
PR 14-SEP-2000; 2000US-0212143.
PR 14-SEP-2000; 2000US-021399.
PR 21-SEP-2000; 2000US-021399.
PR 21-SEP-2000; 2000US-021399.
PR 21-SEP-2000; 2000US-021399.
PR 21-SEP-2000; 2000US-0214274.
PR 21-SEP-2000; 2000US-0214274.
PR 21-SEP-2000; 2000US-021439.
PR 21-SEP-2000; 2000US-021499.
PR 21-SEP-2000; 2000US-02
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The present invention relates to the isolation of novel human uterine motility-association polypeptides, and cDNA (AAS28936-AAS28994) and genomic sequences encoding for these polypeptides.

The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU1804-AAU18152 represent novel human uterine motility-association polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated polypeptide and nucleic acid molecules for treating, preventing and/or prognosing disorders related to uterine motility e.g. disorders associated with pregnancy and the menstrual cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human novel secreted protein, SEQ ID 286.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 11; SEQ ID No 108; 524pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU17045 standard; Protein; 96 AA
                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA, Barash SC, Ruben SM;
                                         2000US-0249245.
2000US-0249245.
2000US-0249265.
2000US-0249265.
2000US-0249297.
2000US-0249297.
2000US-0249300.
                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                        2000US-0250160
                                                                                                                                                                        20000S-0250391
20000S-0251030
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Matches 6; Conservative
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                                                                        17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
27-NOV-2000;
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01-DEC-2000;
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05-DEC-2000;
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δλ
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2000US-0233064.
2000US-0233065.
2000US-0234223.
                                 2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
                                                                              2000US-0235836
                                                                                                                                                                       2000US-0237040
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                                                                      2000US-0235834
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                                                                                                                  2000US-0236369
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                                                                                        2000US-0236327
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2000US-024921
2000US-024921
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                                 21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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29-SEP-2000;
02-OCT-2000;
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08-DEC-2000;
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27-SEP-2000;
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0-OCT-2000
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       vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; carebral isohaemia; angiogenesis; nervous system disorder; hiperproliferation; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
                                                                                                                        17-JAN-2001; 2001WO-US01320
                                                                                                                                                            2000US-0184664
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2000US-0232401
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                                                                                     WO200155441-A2.
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-SEP-2000;
-SEP-2000;
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06-SEP-2000
06-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
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08-SEP-2000
08-SEP-2000
08-SEP-2000
08-SEP-2000
                                                                      Homo sapiens
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                                                                                                                                          31-JAN-2000;
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JS-

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The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunoascays (ELISA). Disorders which are diagnosed or treated inmunoascular disorders e.g. rheumatoid arthritis, cardiovascular disorders e.g. recolars and include autolomnune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, serebrovascular disorders e.g. cardiac arrest, viruses and fungical and occular disorders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other and wound healing and epithelial cell.proliferation, to convent ell and wound healing and epithelial cell.proliferation, to convent ell and wound healing end epithelial cell.proliferation, to convent ell and wound healing and epithelial cell.proliferation.
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                                                                                                                                                                                                                                                                                                      Novel polypeptides and polynucleotides useful as diagnostic reagents to diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein, carbohydrate, vitamins, minerals, cofactors and other nutritional components. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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immune dysfunction; digestive disorder; neoplastic disease;
blood disorder; infectious disease; gene therapy; immunosuppressive;
antiarthritic; cytostatic; vasotropic; antibacterial; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel human calcium-binding protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU19897 standard; Protein; 96 AA.
                                                                                                                                                                                                  Rosen CA, Barash SC, Ruben SM;
                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC.
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54.5%;
08-DEC-2000, 2000US-0251868.
08-DEC-2000; 2000US-0251869.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251999.
                                                                                                             05-JAN-2001; 2001US-0259678
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Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RCLSIXRFXXS 11
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N-PSDB; AAS26950.
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PF 17-JAN-2001; 2001MG-US01302.

RX 31-JAN-2000; 2000US-0180628.

PR 04-FEB-2000; 2000US-0180628.

PR 14-FEB-2000; 2000US-0180628.

PR 15-MAR-2000; 2000US-01806374.

PR 16-MAR-2000; 2000US-0198074.

PR 19-MAR-2000; 2000US-0198074.

PR 19-MAR-2000; 2000US-0198074.

PR 19-MAR-2000; 2000US-0198074.

PR 19-MAR-2000; 2000US-0198074.

PR 18-APR-2000; 2000US-0198074.

PR 19-MAR-2000; 2000US-0198074.

PR 19-MAR-2000; 2000US-0211488.

PR 11-JUL-2000; 2000US-0211488.

PR 11-JUL-2000; 2000US-0211487.

PR 11-JUL-2000; 2000US-0211488.

PR 11-JUL-2000; 2000US-0211488.

PR 11-JUL-2000; 2000US-0211487.

PR 11-JUL-2000; 2000US-021148.

PR 11-JUL-2000; 2000US-021148.

PR 11-JUL-2000; 2000US-021144.

PR 11-JUL-2000; 2000US-0222519.

PR 11-JUL-2000; 2000US-0222919.

PR 11-JUL-2000; 2000US-022919.

PR 11-JUL-2000; 2000US-022919.

PR 11-JUL-2000; 2000US-022919.

PR 11-SEP-2000; 2000US-022919.

PR 11-SEP-2000; 2000US-022399.

PR 11-SEP-2000; 2000US-022399.

PR 11-SEP-2000; 2000US-022399.

PR 11-SEP-2000; 2000US-023399.

PR 21-SEP-2000; 2000US-023399.

PR 21-SEP-2000; 2000US-023399.

PR 21-SEP-2000; 2000US-0233
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The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), disease (e.g. cancer), blood disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. acquired immunodeficiency syndrome, ALDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AVU19892-AAU19969 the invention are also useful in gene therapy. AVU19892-AAU19969 specification, but was obtained in electronic format directly from WIPO
                                           Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                                                                                                                                                                                                                              at ftp.wipo.int/pub/published_pct_sequences
                                                                                         Claim 11; SEQ ID No 94; 542pp; English
 WPI; 2001-465568/50.
                 N-PSDB; AAS31582
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08 NOV - 2000
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05-DEC-2000;
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06-DEC-2000;
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08-DEC-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial; antifungal; vulnerary; antiulcer.
                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bone disorder; osteoporosis; vascular growth disorder;
tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; gene therapy; antiinflammatory;
antiasthmatic; antiarthritic; heemostatic; antiarteriosclerotic;
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                                 DB 22; Length 96;
                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                    Human FLAMINGO 1 homologue, SEQ ID NO:1774.
                                                                     Mismatches
                               34.3%; Score 35; 54.5%; Pred. No.
                                                                                                                                                                                                                             ABB11404 standard; peptide; 2560 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-FEB-2000; 2000US-0496914.
27-APR-2000; 2000US-0560875.
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                                                                                                                                                                                                                                                                                                 11-JAN-2002 (first entry)
                                               Best Local Similarity 54.
                                                                                                    1 RCLSIXRFXXS 11
                                                                                                                       11:1: | | | | 24 RCVSVLRFDSS 34
96 AA;
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Barash SC, Ruben SM;

Rosen CA,

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(HYSE-) HYSEQ INC
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Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49.

N-PSDB; ABA08648

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 20; Page 179-181; 1963pp; English.

chemotractic or chemokinetic activities; chemotractic or chemotractic activities; chemotractic or chemokinetic activities; or may be involved in noncogenesis, cancer cell proliferation or metastasis.

Expending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or ameliorating medical conditions are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Such conditions include cancers, heematopoietic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and retail is chaemia, bone disorders (e.g., osteoporosis), and abnormal vascular for nucleic acids encoding them) may be used to promote wound healing (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders:

Delypeptides with growth factor activity may be used in cell cultures to promote cell growth. For example, such polypeptides may be used to promote cell growth. For example, such polypeptides may be used to manulate or activity may be used to connect the promote cell growth. For example, such polypeptides may be used to connect the promote cell growth or activity may be used to connect the promote cell growth or activity may be used to cell culture to give rise to neuroepithelial cells the parameters. Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABA0825-ABA09574 represent nucleic acids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleotide of the invention, methods of producing the novel polypeptides, antibodies against the polypeptides, methods of detecting the nucleotides or polypeptides in a sample, and methods of identifying compounds which bind to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential therapeutic applications. The polypeptides of the invention may differentiation activities, including cytokine, cell proliferation or cell havematopoiesis regulatory activity; issue growth activity; immunomodulatory activity; activing or inhibin-related activities; that can be used to augment or replace cells damaged by illness, autoimmune disease or accidental damage. The polypeptides and nucleotides may also be used in the diagnosis of the above conditions, and in drug screening techniques. The present sequence represents a novel human polypeptide of the invention.

2560 AA; Sequence

Gaps ó 34.3%; Score 35; DB 22; Length 2560; 54.5%; Pred. No. 2.2e+02; ive 2; Mismatches 3; Indels (Conservative Query Match Best Local Similarity Matches 6; Conserva

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1 RCLSIXRFXXS 11

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Search completed: July 16, 2003, 17:46:43 Job time : 10.9578 secs

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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
WUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED AND BERRY
6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 7.7e-08;
0; Mismatches 15;
                                                            US-08-467-9488-30
US-08-467-9488-30
US-08-467-9478-30
US-08-467-9488-8
US-08-467-9478-8
US-08-467-9478-8
US-08-417-129A-6
US-08-417-122-6
US-08-417-122-6
US-08-417-122-6
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US-08-541-759B-2
US-08-134-638-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 210121.426C1 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 32, Application US/08845258 Patent No. 6183976 GENERAL INFORMATION:
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ATTORNEY/AGENT INPORMATION:
NAME: Maki, David J. REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Washington
COUNTRY: USA
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being printed,
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score greater than.or equal to the score of the result bein
and is derived by analysis of the total score distribution.
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-08-723-142A-32
US-08-952B-784A-32
US-08-990-571-36
US-09-52B-744A-36
US-09-52B-744A-36
US-09-58-744A-36
US-09-574-141A-64
US-09-182-616-4
US-09-182-616-4
US-08-352-674-17
US-08-352-674-4
US-08-352-674-4
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US-09-574-141A-66
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US-09-574-141A-66
US-09-674-141A-66
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1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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US-08-816-241-5
US-09-040-482-5
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Paul R.
APPLICANT: Geath, Paul R.
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42664
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                          Score 75; DB 4; Length 245;
Pred. No. 7.7e-08;
0; Mismatches 15; Indels
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PatentIn Release #1.0, Version #1.30
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53.1%; Pred. No. 7.7e-08;
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                                                                                                                                                                  210121.426
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Patent No. 6183976
              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, DAVIG J.
REGISTRATION NUMBER: 2101:
TELECHONE: (206) 622-4900
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                              73.5%;
53.1%;
                                                                                                                                                                                                                       TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 245 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 73.55
Best Local Similarity 53.15
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.5
Best Local Similarity 53.1
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                       linear
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APPLICANT: Reed,
                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY:
US-08-723-142A-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-528-784A-32
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                                                                  Sequence 32, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                         ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Waki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/08723142A Patent No. 6306396
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ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPATIBLE
PC-DOS/MS-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206)682-6231
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 245 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 53.1:
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: SEED AND STREET: 6300 Columb CITY: Seattle STATE: Washington
                                                                                                                                                                                                                                                                                   STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                           98104
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US-08-723-142A-32
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US-08-990-571-32
                                                       US-08-990-571-32
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us-09-853-079-36.rai

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MAME/KEY: Modified-site
LOCATION: 21
OTHER INFORMATION: /note= "Residue can be either Ala
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OTHER INFORMATION: or Ile"
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OTHER INFORMATION: or Ser"
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OTHER INFORMATION: /note= "Residue can be either Ile
OTHER INFORMATION: or Phe"
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OTHER INFORMATION: or Ile"
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OTHER INFORMATION: or Arg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note= "Residue can be either OTHER INFORMATION: or Phe"
                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/845,258 FILING DATE: 24-APR-1997 CLASSIFICATION: 435
                 ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Residue can be Pro,
Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210121.426C1
                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site LOCATION: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
CORRESPONDENCE ADDRESS:
                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: 13
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                     COUNTRY: U
ZIP: 98104
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APPLICANT: Reed, Steven G. et al.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Scattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70.6%; Score 72; DB 4; Length 32; 100.0%; Pred. No. 4.1e-08; ive 0; Mismatches 0; Indels
                                                                             /note= "Residue can be either Leu
or Pro"
                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /note= "Residue can be either Val
OTHER INFORMATION: or Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: /note= "Residue can be either Cys; OTHER INFORMATION: Or Tyr" US-08-845-258-36
                                                                                                                                                                    LOCATION: 26
OTHER INFORMATION: /note= "Residue can be either Met
OTHER INFORMATION: or Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Residue can be either Thr
or Ile"
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: TBM PC COMPATIBLE
COMPUTER: PACHELINE PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: II-DEC-1997
CLASSIFICATION:
ATTONREY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 31,392
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHANE: (206) 622-4900
TELEFRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                     /note= "Residue can be either or Leu"
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OTHER INFORMATION: or Val"
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LOCATION: 29
OTHER INFORMATION: /note
OTHER INFORMATION: or il
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    NAME/KEY: Modified-site
    LOCATION: 30
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27
                                          Modified-site
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Best Local Similarity 100.0'
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LOCATION: 27
OTHER INFORMATION: OTHER INFORMATION: OFFEATURE:
                                                                               OTHER INFORMATION:
OTHER INFORMATION:
EATURE:
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US-08-990-571-36
                                                                LOCATION:
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/note= "Residue can be Pro, Ser or
Leu"
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                                                                                                                                                  /note= "Residue can be either Met or Ile"
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or Phe"
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or Val"
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or Pro"
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or Phe"
                                                                                                                                                                                                                                           /note= "Residue can be either Tyr
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Residue can be either or Ile"
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or Phe"
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                                                                                                                                                                                                                                                           or Ser"
                                                                                                                                                                                                                                                                                         NAME/KEY: Modified-site
LCCATION: 10
OTHER INFORMATION: /note-
OTHER INFORMATION: Or Phe
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
                                                                                                 FEATURE:
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note=
OTHER INFORMATION: or lle
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NAME/KEY: Modified-site
LOCATION: 19
OTHER INFORMATION: /note=
OTHER INFORMATION: Gly"
FEATURE:
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NAME/KEY: Modified-site
LOCATION: 17
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NAME/KET: Modified-site
LOCATION: 9
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LOCATION: 13
OTHER INFORMATION: /note
OTHER INFORMATION: Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site LOCATION: 21
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NAME/KEY: Modified-site
LOCATION: 26
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LOCATION: 28
OTHER INFORMATION: /note
OTHER INFORMATION: or Ph
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LOCATION: 20
OTHER INFORMATION: /not.
OTHER INFORMATION: or P
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                      TOPOLOGY: linear
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                       Query Match 70.6%; Score 72; DB 4; Length 32; Best Local Similarity 100.0%; Pred. No. 4.1e-08; Matches 32; Conservative 0; Mismatches 0; Indels
               /note= "Residue can be either Thr or Ile"
                                                                                                                        /note= "Residue can be either Cys
or Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= "Residue can be either Met
OTHER INFORMATION: or Ile"
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or Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 21,32
REFERENCE/DOCKET NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 36, Application US/08723142A Patent No. 6306396
LOCATION: 29
COTHER INFORMATION: /note==
COTHER INFORMATION: or Ile"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30
COTHER INFORMATION: /note==
COTHER INFORMATION: or Tyr"
US-08-990-571-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: 9
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY:
LOCATION:
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US-08-723-142A-36
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS 90
SOFTWARE: FASTESQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Methionine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa - Serine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Leucine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = Tyrosine or Serine
                                               Sequence 36, Application US/09528784A Patent No. 6451315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Babesia microti
                                                                                                    GENERAL INFORMATION:
APPLICANT: Reed, St.
APPLICANT: Lodes, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT LOCATION: (13)...
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                          -09-528-784A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Residue can be either Ile
OTHER INFORMATION: or Phe"
OTHER INFORMATION: /note= "Residue can be either Ser
OTHER INFORMATION: or Phe"
                                                                                                                   OTHER INFORMATION: /note= "Residue can be either Leu
OTHER INFORMATION: or Ile"
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OTHER INFORMATION: or Val"
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OTHER INFORMATION: or Pro"
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or Thr"
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or Phe"
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OTHER INFORMATION: /note= "Residue can be either Thr
OTHER INFORMATION: or Ile"
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                /note= "Residue can be either Leu
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NAME/KEY: Modified-site
LOCATION: 27
OTHER INFORMATION: /note= "Residue can be either
OTHER INFORMATION: or Leu"
                                                                                                                                                                                                                                               OTHER INFORMATION: /note= "Residue can be Pro, OTHER INFORMATION: Leu"
                                                                                                                                                                                                                                                                                                                                                                                                        or Arg"
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NAME/KEY: Modified site
LOCATION: 20
LOCATION: 20
                                                                       NAME/KEY: Modified-site LOCATION: 12
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NAME/KEY: Modified-site
LOCATION: 19
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LOCATION: 28
OTHER INFORMATION: /note
OTHER INFORMATION: or Ph
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OTHER INFORMATION:
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LOCATION:
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Gaps
                                                                                                                      NAME/KEY: VARIANT
LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = Glutamic Acid, Aspartic Acid or Glycine
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                                                                                                                                                                                         NAME/KEY: VARIANT LOCATION: (20)...(20) OTHER INFORMATION: Xaa = Isoleucine or Phenylalanine
LOCATION: (13)...(13)
OTHER INFORMATION: Xaa = Proline, Serine or Leucine
NAME/KEY: ANTANAT
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa = Leucine or Arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 70.6%; Score 72; DB 4; Le
Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Methionine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Threonine or Isoleucine
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa = Valine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (30)...(30)
; OTHER INFORMATION: Xaa = Cysteine ro Tyrosine
US-09-528-784A-36
                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Leucine or Proline
                                                                                                                                                                                                                                                                                              LOCATION: (21)...(21)
OTHER INFORMATION: Xaa = Alanine or Valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: (27)...(27)
OTHER INFORMATION: Xaa = Serine or Leucine
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                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT
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Query Match
Best Local Similarity
Matches 7; Conserva
                                                                                              OPERATING SYSTEM:
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STRANDEDNESS: sin
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                                                                                 COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
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                                                                                                                                                                                              APPLICANT: Fukudome, Kenji
APPLICANT: Esmon, Charles T.
TITLE OF INVENTION: Cloning and Regulation of an Endothelial
TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
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Patent No. 585271
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fukudome, Kenji
APPLICANT: Esmon, Charles T.
TITLE OF INVENTION:
CIOLING and Regulation of an Endothelial
TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
STREET: Street
                                                                                                                                                                                                                                                                                                                                     STREET: 2800 One Atlantic Center, 1201 West Peachtree STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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30;
RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                  1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXFL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/289,699A FILING DATE: 12-AUG-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OMRF152
                                                                                                                                Sequence 4, Application US/08289699A Patent No. 5695993 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
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50.0%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 30306-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L.
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                US-08-289-699A-4
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Gaps
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Patent No. 6399064
GENERAL INFORMATION:
APPLICANT: Fukudome, Kenji
APPLICANT: Fukudome, Kenji
TITLE OF INVENTION: Cloning and Regulation of an Endothelial
Cell Protein C/Activated Protein C Receptor
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ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 335;
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                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
30;
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FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: OMRF152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33;
                                                                                                                                                    FILING DATE:
CLASSIFCTATION: 424
PRIOR APPLICATION DATA:
RAPLICATION NUMBER: US 08/289,699
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
                                                                                                                                   APPLICATION NUMBER: US/08/878,283
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                                                                                                                                                                                                                                                                                                                               OMRF152
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ZIP: 30306-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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                                                IBM PC compatible
                                                                                                                                                                                                                                                                                     NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31,284 REFERENCE/DOCKET NUMBER: OM
                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION TELEPHONE: (404)873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.4%;
50.0%;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                          (404)873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29 RCLQISSFANSSWT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                            335 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RCLSIXRFXXSXXT 14
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Atlanta
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                                                                                          Gaps
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                                               DB 3; Length 348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/08352678

Patent No. 6043351

GENERAL InfoRMATION:
GENERAL InfoRMATION:
TITLE OF INVENTION: BESTEIN BARR VIRUS INDUCED GENES
ITLE OF INVENTION: BESTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Epstein Barr Virus Induced Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750 FILING DATE: Herewith CLASSIFICATION: 43f ATTORNEY/APPLICATION: 43f
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach
Interfor Interfor
INMER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
STREET: Suite 600
CITY: Washington
STATE: D.C.
                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627.3300001
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                               Score 31;
Pred. No. 8
                                                                                                                                                                                                                                                              US-08-383-750-4; Sequence 4, Application US/08383750; Patent No. 5744301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
                                             Query Match 30.4%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 30.4
Best Local Similarity 85.7
Matches 6; Conservative
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                                                                                                                                                             |||| ||
121 CLSIDRF 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 CLSIXRF 8
                                                                                                                                  2 CLSIXRF 8
    US-08-852-824-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Gonsalves, Dennis
APPLICANT: Gonsalves, Dennis
APPLICANT: Gonsalves, Dennis
TITLE OF INVENTION: WUPESTRIS STEM PITTING ASSOCIATED VIRUS
TITLE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
FILE REPERRENCE: 07678/038005
CURRENT APPLICATION NUMBER: 05/09/574,141A
CURRENT APPLICATION NUMBER: 60/047,147
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069,902
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 09/081,320
PRIOR APPLICATION NUMBER: 09/081,320
PRIOR FILING DATE: 1998-05-19
NUMBER OF SEQ ID NOS: 97
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 64
                                                                                                                                                                                                                                                                                   DB 4; Length 335; 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; DB 4; Length 379;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12; Indels
                                                                                                                                                                                                                                                                                                                                7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 17. Application US/08852824C
Patent No. 6060272
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Human G-Protein Coupled Receptors FILE REFERENCE: 1488.1220000
CURRENT APPLICATION NUMBER: US/08/852,824C
CURRENT FILING DATE: 1997-05-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Rupestris stem pitting associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 32.4%; Score 33; DB Best Local Similarity 33.3%; Pred. No. 34; Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                     Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
US-09-574-141A-64
: Sequence 64, Application US/09574141A
; Patent No. 6395490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 AIMRFSGEASTFLNTLANMLF 248
TELECOMMUNICATION INFORMATION
                      TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 SIXRFXXSXXTFIXIXXXMXF 24
                                                                                                       LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                   32.4%;
                                                                                                                                                                                                                                                                                                                                                                        1 RCLSIXRFXXSXXT 14
                                                                                                                                                                                                                                                                                                                                                                                                               29 RCLQISSFANSSWT 42
                                                                                                                                                                                                                                                                                                                                7; Conservative
                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-574-141A-64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-852-824-17
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LENGTH: 348
                                                                                                                                                                                                                                        US-09-182-616-4
                                                                                                                                                                                                                                                                                     Query Match
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STATE: WA
COMPUTER: LUSA
ZIP: 0210
COMPUTER: LOPPY disk
MEDIUM TYPE: Floppy disk
COMPUTER: TEMPORALIBE FORM:
COMPUTER: TEMPORALIBE
COMPUTER: TEMPORALIBE
COMPUTER: TEMPORALIBE
COMPUTER: TEMPORALIBE
COMPUTER: TEMPORALIBE
COMPUTER: TEMPORALIBE
COMPUTER: 30-NOV-1994
CUASSIFICATION NUMBER: US/08/352,678
FILING DATE: 30-NOV-1994
CUASSIFICATION NUMBER: US/07/980,518
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CALERANCE/CONCET UNMBER: B0801/7044
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acid
TOPOLOGY: 11near
TOPOLOGY: Linear
```

Search completed: July 16, 2003, 17:50:59 Job time : 3.914 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:47:39 ; Search time 5.2344 Seconds Run on:

(without alignments)
726.026 Million cell updates/sec

US-09-853-079-36 102 1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32

Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

451899 seqs, 118759770 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

/cgn2_6/ptodata/2/pubpaa/US06_PUBGOMB.pep:*/cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US01_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US08_PUBW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*/ /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_UBUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:* /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:* /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ď				
Result		Query				
NO.	Score	Match	Match Length DB	DB	UD	Description
1	75	73.5		6	US-09-286-488-32	Sequence 32, Appl
7	75	73.5	245	6	US-09-853-079-32	Sequence 32, Appl
m	75	73.5		10	US-09-737-178-32	Sequence 32, Appl
4	72	70.6	32	σ	US-09-286-488-36	Seguence 36, Appl
S	72	70.6	32	Q	US-09-853-079-36	Sequence 36, Appl
9	72	70.6	32	10	US-09-737-178-36	Sequence 36, Appl
7	35	34.3	96	σ	US-10-073-865-108	Sequence 108, App
80	35	34.3		σ	US-09-764-881-94	Sequence 94, Appl
6	35	34.3	96	10	US-09-764-853-659	Sequence 659, App
10	35	34.3		10	US-09-764-898-286	Sequence 286, App
11	35	34.3		6	US-09-916-849A-3	Sequence 3, Appli
12	35	34.3	2923	σ	US-10-225-567A-524	Sequence 524, App
13	35	34.3		10	US-09-788-711A-4	Sequence 4, Appli
14	35	34.3		10	US-09-788-711A-2	Sequence 2, Appli
15	34	33.3		10	US-09-764-864-996	Sequence 996, App
16	33	32.4		σ	US-10-156-761-12232	Sequence 12232, A
17	32	31.4		10	US-09-737-149-27	Sequence 27, Appl
18	32	31.4		σ	US-10-225-567A-444	Sequence 444, App
19	32	31.4	3014	10	US-09-737-149-2	Sequence 2, Appli

Sequence 32, Application US/09853079 Publication No. US20030109689A1 GENERAL INFORMATION: APPLICANT: Reed, Steven G.

RESULT 2 US-09-853-079-32

Lodes, Michael J. Houghton, Raymond L. Sleath, Paul R. McNeill, Patricia D.

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

A 7 4 7 4 7 4 7 4 7 4 7 4 7 4 7 4 7 4 7	sequence 300, App Sequence 306, App Sequence 5603, Ap Sequence 812, App Sequence 4443, Ap
10 US-09-737-149-25 9 US-10-149-30 9 US-10-149-30 9 US-10-125-567A-656 10 US-09-737-149-29 10 US-09-737-149-29 10 US-09-827-937A-17 9 US-10-22-0377-17 9 US-10-251-385-206 9 US-10-251-385-206 9 US-10-251-385-206 10 US-09-864-761-47425 9 US-10-083-357-121 10 US-09-864-761-38466 10 US-09-864-761-38466	9 US-1U/4-035-306 10 US-09-764-860-306 9 US-10-106-698-5603 9 US-09-925-299-812 9 US-10-106-698-4443
3034 3034 33034 3312 3313 3402 3402 361 417 70 422 422 423 431 1734 361 361 361 361 361 361 361 361 361 361	8 8 6 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5
11111100000000000000000000000000000000	27.5 27.5 27.5 27.5 27.5
25	8 8 8 8 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7
01000000000000000000000000000000000000	4444 4443 243

ALIGNMENTS

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
0
                                                                                      GENERAL INPORTORIES

APPLICANT: Reed, Steven G.

APPLICANT: LOGGS, Michael J.

APPLICANT: Lodge, Michael J.

APPLICANT: Sleath, Paul R.

APPLICANT: Monitor Raymond L.

APPLICANT: Monitor Raymond L.

APPLICANT: Monitor Raymond L.

TITLE OF INVENTION: COMPOUNDS MD METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: COMPOUNDS

FILE REFERENCE: 210121.4263

CURRENT APPLICATION NUMBER: US/09/286,488

CURRENT FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 32

LENGTH: 245

TYDE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%; Score 75; DB 9; Let 53.1%; Pred. No. 2.1e-07; iive 0; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                               Sequence 32, Application US/09286488 Patent No. US20020169136A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.5
Best Local Similarity 53.1
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Babesia microti
US-09-286-488-32
RESULT 1
US-09-286-488-32
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Gaps
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INFORMATION: Xaa = Glutamic Acid, Aspartic Acid or Glycine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ION: (20)...(20)
INFORMATION: Xaa = Isoleucine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (13)...(13)
INFORMATION: Xaa = Proline, Serine or Leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                      LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Methionine or Isoleucine
                                                                                                                                                                                                                                                                                                                               ION: (10)...(10)
INFORMATION: Xaa = Serine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ION: (26)...(26)
INFORMATION: Xaa - Methionine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ION: (28)...(28)
INFORMATION: Xaa = Valine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Threonine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 72; DB 9; I
Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                              ION: (12)...(12)
INFORMATION: Xaa = Leucine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COCATION: (30)...(30)
CTHER INFORMATION: Xaa = Cysteine ro Tyrosine US-09-286-488-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.6%; bcc. 100.0%; Pred. No. 1... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LON: (17)...(17)
INFORMATION: Xaa = Leucine or Arginine
                                                                                                                                                                                                                                                                      - Tyrosine or Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Leucine or Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (27)...(27)
OTHER INFORMATION: Xaa = Serine or Leucine
          NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 70.6 Best Local Similarity 100. Matches 32; Conservative
                                                                                                          ORGANISM: Babesia microti
                                                                                                                                                                                                                                                    ION: (9)...(9)
INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CON: (21)...(21)
INFORMATION: Xaa
                                                                                                                                                                                                                               NAME/KEY: VARIANT
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Pred. No. 2.1e-07;
D: Mismatches 15; Indels
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS-
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS-
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 245
                                                                                                                                                                                                                                                                                                            Length 245;
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: MONELIL, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.4263
CURRENT APPLICATION NUMBER: US/09/286,488
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2.1e-07;
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CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                            Score 75;
Pred. No.
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Lodes, Michael J.
Houghton, Raymond L.
Sleath, Paul R.
McNeill, Patricia D.
Homer, Mary
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53.1%;
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US-09-853-079-32
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US-09-737-178-32
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SOFTWARE: FastSEQ for
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Best Local Similarity
Matches 17; Conserv
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LENGTH: 245
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Best Local
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APPLICANT:
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LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = Glutamic Acid, Aspartic Acid or Glycine
FEATURE:
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Moner, Mary
APPLICANT: Gently, Paul R.
APPLICANT: Gently, Paul R.
APPLICANT: Gently, Paul R.
APPLICANT: Morey, Mary
APPLICANT: Compounds AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 2012.12.426611
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001.05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 32
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OTHER INFORMATION: Xaa = Isoleucine or Phenylalanine
FEATURE:
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INFORMATION: Xaa = Proline, Serine or Leucine
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OTHER INFORMATION: Xaa - Methionine or Isoleucine
FEATURE:
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OTHER INFORMATION: Xaa = Methionine or Threonine
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OTHER INFORMATION: Xaa = Serine or Phenylalanine
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OTHER INFORMATION: Xaa - Leucine or Isoleucine
1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXFL 32
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OTHER INFORMATION: Xaa = Leucine or Arginine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa - Tyrosine or Serine
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OTHER INFORMATION: Xaa = Leucine or Proline
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OTHER INFORMATION: Xaa = Alanine or Valine
                                                                                                                           US-09-853-079-36
; Sequence 36, Application US/09853079
; Publication No. US20030109689A1
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LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = Glutamic Acid, Aspartic Acid or Glycine
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APPLICANT: Sleath, Paul R.
APPLICANT: Graft, Patricia D.
APPLICANT: Homer, Mary Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426c9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 36
LENGTH: 32
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LOCATION: (20)...(20)
OTHER INFORMATION: Xaa = Isoleucine or Phenylalanine
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OTHER INFORMATION: Xaa = Proline, Serine or Leucine
NAME/KEY: VARIANT
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LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Methionine or Isoleucine
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OTHER INFORMATION: Xaa = Serine or Phenylalanine
                                                                                                     LOCATION: (28)....(28)
OTHER INFORMATION: Xaa - Valine or Phenylalanine
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OTHER INFORMATION: Xaa = Threonine or Isoleucine
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OTHER INFORMATION: Xaa - Leucine or Isoleucine
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NAME/KEY: VARIANT
LOCATION: (30)...(30)
CYTER INDEMATION: Xaa = Cysteine ro Tyrosine
US-09-853-079-36
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OTHER INFORMATION: Xaa = Leucine or Arginine
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LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = Tyrosine or Serine
LOCATION: (27)...(27)
OTHER INFORMATION: Xaa = Serine or Leucine
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APPLICANT: Reed, 5
                                                  FEATURE: NAME/KEY: VARIANT
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LENGTH: 96
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                                                                                                                                                                                                                     FEATURE:
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; Publication No. US20030044904A1
; GENERAL INFORMATION:
; APPLICANT: ROSen et al.
; TITLE OF INVENTION:
; FILE REFERENCE: PJZ09C1
; CURRENT FALLIGATION NUMBER: US/10/073,865
; CURRENT FILIG DATE: 2002-02-14
; Prior Application removed - See file Wrapper or Palm
; NUMBER OF SEQ ID NOS: 154
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 70.6%; Score 72; DB 10; I Best Local Similarity 100.0%; Pred. No. 1.2e-07; Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                 LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Methionine or Threonine
                                                                                                                                                                                                                                                    LOCATION: (28)...(28)
OTHER INFORMATION: Xaa = Valine or Phenylalanine
                                                                                                                                                                                                                                                                                                          LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Threonine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: VARIANT
LOCATION: (30)...(30)
STER INFORMATION: Xaa - Cysteine ro Tyrosine
US-09-737-178-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                        LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Leucine or Proline
NAME/KEY: VARIANT
                                                                                                                                                                                 LOCATION: (27)...(27)
OTHER INFORMATION: Xaa = Serine or Leucine
NAME/KEY: VARIANT
                    LOCATION: (21)...(21)
OTHER INFORMATION: Xaa = Alanine or Valine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 94, Application US/09764881; Publication No. US20030125246A9; GENERAL INFORMATION:
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LOCATION: (89)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: (92)
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ORGANISM: Homo sapiens
                                                          NAME/KEY: VARIANT
                                                                                                                                                                         NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                    OTHER INFORMATION NAME/KEY: VARIANT
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US-09-764-881-94
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LOCATION: (89)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (92)
LOCATION: (92)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-94
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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FILE REFERENCE: PIZO7

CURRENT APPLICATION NUMBER: US/09/764,881

CURRENT FILID DATE: 2001-01-17

Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 94

LENGTH: 96
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Pred. No. 8.2;
2; Mismatches 3; Indels
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PUZON
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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Patent No. US20020090673A1
GENERAL INFORMATION
THEORY TROSEN et al.
TITLE OF INVERMION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PIZO1
CURRENT APPLICATION NUMBER: US/09/764,898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB 9; Length 96;
Pred. No. 8.2;
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; Patent No. US20020090672A1
; GENERAL INFORMATION:
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54.5%;
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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Matches 6; Conservative
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24 RCVSVLRFDSS 34
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Pred. No. 2.1e+02;
2; Mismatches 3; Indels
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Pred. No. 2.1e+02;
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Pred. No. 2.1e+02;
2; Mismatches 3
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APPLICANT: Tania Tamsin Testa
TITLE OF INVENTION:
FILE REFERENCE: GP-30225
CURRENT APPLICATION NUMBER: US/09/788,711A
CURRENT FILING DATE: 2001-02-20
PRIOR FILING DATE: 2000-02-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                               2; Mismatches
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TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30225
CURRENT APPLICATION NUMBER: US/09/788,711A
CURRENT FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09788711A Patent No. US20020058328A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 0004196.2
PRIOR FILING DATE: 2000-02-19
                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/09788711A Patent No. US20020058328A1
                                                                                                                                       34.3%;
54.5%;
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54.5%;
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54.5%;
      SOFTWARE: PatentIn version 3.1
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|1242 RCVSVLRFDSS 1252
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1242 RCVSVLRFDSS 1252
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Matches 6; Conservative
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                                                                              ; ORGANISM: Homo sapiens
US-10-225-567A-524
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Matches 6; Conserv
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Matches 6; Conserv
                        SEQ ID NO 524
LENGTH: 2923
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US-09-788-711A-4
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US-09-788-711A-2
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LENGTH: 2956
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                                                                TYPE: PRT
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APPLICANT: Brown, Joseph P.
APPLICANT: Burmer, Glanna C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/09916849A
Bublication No. US20030086934A1
GENERAL INFORMATION.
GENERAL INFORMATION.
APPLICAMY: Bostein, et al.
TITLE OF INVENTION: Basal Markers in Breast Cancer and Related Reagents
TITLE OF INVENTION: USes Thereof
FILE REPERENCE: 2002850-0024
CURRENT APPLICATION NUMBER: US/09/916,849A
CURRENT FILING DATE: 2001-07-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 286
LENGTH: 96
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Pred. No. 2.1e+02;
2; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                                  34.3%;
54.5%;
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54.58;
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Best Local Similarity 54.5°
""has 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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24 RCVSVLRFDSS 34
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                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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US-10-225-567A-524
                                                                                                                                                                                                                                    NAME/KEY: SITE LOCATION: (92)
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LENGTH: 2923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-916-849A-3
                                                                                                                                                                                               LOCATION:
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RESULT 15

US-09-764-864-996

Sequence 996, Application US/09764864

Patent No. US20020132753a1

GENERAL INFORMATION:

TITLE OF INVENTATION: Nucleic Acids, Proteins, and Antibodies

FILE REPRENEE: PT23

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT PELING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper

NUMBER OF SEQ ID NOS: 1792

SEQ ID NO 996

LENGTH: 359

CORTWARR: Patentin Ver. 2.0

SEQ ID NO 966

LENGTH: 359

CORGANISM: Homo sapiens

US-09-764-864-996

QUETY MATCH

Best Local Similarity 37.5%; Pred. No. 45;

Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps

OY 1 RCLSIXREXXXXTF1 16

II: 11

Db 105 RCIECGKFLKKHSTF1 120

Search completed: July 16, 2003, 18:08:35

JOB time: 6.2344 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

July 16, 2003, 17:50:14; Search time 3.7774 Seconds (without alignments) 814.396 Million cell updates/sec

Title:

US-09-853-079-36 102 1 RCLSIXRFXXSXXFIXIXXXMXFFXXXXXFL 32 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		dР			SUMMARIES	
Result No.	Score	Query	Query Match Length	DB	ID	Description
П		35.3	234	~	T47553	peroxiredoxin-like
7	36	S.	376	~	G71290	flagellar biosynth
m		34.3	208	~	T20554	hypothetical prote
4		34.3	116	7	T20896	
2	34	33.3	106	~	H83754	S
9	33	32.4	335	-	HLHUR3	T-cell surface qly
7		32.4	393	7	G86725	hypothetical prote
æ		32.4	513	7	.T37806	>
σ	33	32.4	670	~	T33304	hypothetical prote
10	32.5	31.9	312	ď	T20668	
11	32	31.4	297	7	C71675	
12	32	31.4	373	N	D89865	
13	32	31.4	492	7	E58931	ŏ
14	32	31.4	512	~	H86832	hypothetical prote
15	32	31.4		7	T14119	seven-pass transme
16	31.5	30.9		7	T34417	delayed rectifier
17	31	30.4	194	7	T22209	hypothetical prote
18	31	30.4	226		A98058	conserved hypothet
19	31	30.4	264		S75501	hypothetical prote
50	31	30.4	317		H97143	probable membrane
21	31	30.4	361		B45680	G protein-coupled
22	31	30.4	.370		T04664	hypothetical prote
23	31	30.4	517		T20174	hypothetical prote
24	31	30.4	558		T23991	_
25	31	30.4	617	~	T22175	hypothetical prote
26	31	30.4	977	ď	H84469	_
27	31	30.4	1010	N	T36383	probable large ATP
28	30	29.4	93	~	T10294	ubiquitin-like pro
29	30	29.4	93	7	JQ2029	ubiquitin - Orgyia

hypothetical prote	hypothetical prote	hypothetical prote	prophage pi3 prote	hyporhetical prote	hypothetical prote	hypothetical prote	3',5'-cyclic-nucle	protein C18B10.8 (probable presenili	hypothetical prote	probable membrane	hypothetical prote	hypothetical prote
S59333 S53852	T16518	G97831	н86803	T193/3	T17764	T20648	A40602	н89102	A84702	S11961	D95947	T18782	T21184
4.2	77	4 (1	~	٦.	7	N	7	7	~	7	7	7	7
112	217	266	283	304	314	327	330	364	397	411	417	523	532
29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4
30	30	30	30	30	30	30	30	30	30	30	30	30	30
30	32	34	35	36	37	38	36	40	41	42	43	44	45

ALIGNMENTS

pr-2000 eichselgartner,	Gaps 0;
REGULT 1 147536 1747536 1747536 1747536 1747536 1747536 17586cies: Arabidopsis thaliana N; Alternate names: protein F8J2.130 17586cies: Arabidopsis thaliana (mouse-ear cress) 17586cies: Arabidopsis thaliana, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, 178978 A.; E. X. 17896 Salva (17896) 17896 Salva (1	Similarity 43.8%; Score 36; DB 2; Length 234; 7; Conservative 2; Mismatches 7; Indels 0; Gaps LSIXRFXXSXXTFIX 18 : : LSVSRFMSSSATVISV 20
RESULT 1 T47553 peroxiredoxin-like N; Alternate names C; Species: Arabid C; Date: 20-Apr-201 C; Accession: T475; R; Nyakatura, G; Mayer, K.F.X. submitted to the 1 A; Reference number A; Accession: T475; A; Status: prelimila A; Molecule type: 1 A; Residues: 1-234 A; Cross-reference A; Accoss-reference A; Cross-reference A; Cross-refere	Query Match Best Local Matches Qy 3

flagellar biosynthetic protein flhB homolog TP0715 - syphilis spirochete C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 05-Nov-1999
C; Accession: G71290; PC4115
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; G
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; M
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A; Reference number: A71250; MUD: 98332770; PMID: 9665876
A; Reference number: acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-376 <CCL>
A; Cross-references: GB: AE001244; GB: AE000520; NID: 93323005; PIDN: AAC65681.1; PID: 9332
A; Experimental source: strain Nichols
A; Cross-references: GB: AE001244; GB: AE000520; NID: 93529894
A; Title: Identification and sequences of the Treponema pallidum flim', flip, flip, fl

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7 REXXSXXTEIXIXXXMXFF 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 33.3%;
Best Local Similarity 42.1%;
Matches 8; Conservative 1
                                                                                                                                             Query Match
Best Local Similarity 33.33
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Superfamily: sugE protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BH0840
                C; Genetics:
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A;Accession: PC4115
A;Molecule type: DNA
A;Residues: 1-312 <HAR>
A;Residues: 1-312 <HAR>
A;Cross_references: GB:U36839; GB:U26453; NID:g1216381
C;Comment: This protein is a member of a gene complex involved in the biogenesis and asserport of flagellar protein or virulence factor.
                                                                                                                                                                C;Genetics:
A;Gene: filhB; TPO715
A;Gene: filhB; TPO715
C;Superfamily: flagellar biosynthetic protein flhB; flhB carboxyl-terminal homology C;Keywords: inner membrane
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C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20896
R;Lightning, J.
submitted to the EMBL Data Library, October 1995
A;Reference number: 219342
A;Reference number: 219342
A;Recession: T20896
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-776 <WIL>
A;Residues: 1-776 <WIL>
A;Cross-references: EMBL: 254307; PIDN: CAA91092.1; GSPDB: GN00020; CESP: F14F11.1
A; Experimental source: clone F14F11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-208 <W12>
A;Cross-references: EMBL:270755; PIDN:CAA94786.1; GSPDB:GN00023; CESP:F07D3.2
A;Experimental source: clone K06A4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-208 <WIL>
A; Cross-references: EMBL:271179; PIDN:CAA94889.1; GSPDB:GN00023; CESP:F07D3.2
A; Experimental source: clone F07D3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F07D3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20554; T23359
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                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, April 1996
A; Reference number: 219291
A; Accession: 720554
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.3%; Score 35; DB 2; 40.0%; Pred. No. 4.6; ative 3; Mismatches
                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 CIGVLRFFFTRATTASIONTGWFFVFVRYFM 105
                                                                                                                                                                                                                                                                                                     Score 36; DB Pred. No. 4.7; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          2 CLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, April 1996 A; Reference number: 219731 A; Accession: T23359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Introns: 37/3; 66/1; 127/2; 150/2; 182/2
                                                                                                                                                                                                                                                                                                   Query Match 35.3%;
Best Local Similarity 25.8%;
Matches 8; Conservative
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Best Local Similarity
6, Conserve
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T-cell surface glycoprotein CD1d precursor - human
N; Alternate names: T-cell surface glycoprotein CD1.R3; thymocyte differentiation anti
C; Species: Homo sapiens (man)
C; Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Ju1-2000
C; Accession: S07715; A32217; I79469; A30599
R; Calabi, F.; Jarvis, J.M.; Martin, L.; Milstein, C.
Eur. J. Immunol. 19, 285-292, 1989
A; Title: Two classes of CD1 genes
A; Reference number: A30599; MUID:89196496; PMID:2467814
A; Reference number: BNA
A; Residues: 1-335 cCAL>
A; Residues: EMBL:X14974; NID:g29767; PIDN:CAA33099.1; PID:g4539529
A; Tross-references: EMBL:X14974; NID:g29767; PIDN:CAA33099.1; PID:g4539529
A; Experimental source: clone lambda R3G1
R; Balk, S. P.; Blaicher, P.A.; Terhorst, C.
Proc. Natl. Acad Sci. U.S.A. 86, 252-256, 1989
A; Accession: A32217; MUID:89098892; PMID:2463622
A; Accession: A32217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multidrug resistance protein BHO840 [imported] - Bacillus halodurans (strain C-125) (Species: Bacillus halodurans (strain C-125) (Species: Bacillus halodurans (species: Bacillus halodurans (Spacession: H83754 (Spate: Old) (Sequence_revision Ol-Dec-2000 #text_change 15-Jun-2001 (Spacession: H83754 (Makasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H Nucleic Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A; Reference number: A83550; MUID:20512582; PMID:11058132 (MASSATUR: preliminary A; Molecule type: DNA A; Status: preliminary A; Molecule type: DNA A; Residues: 1-106 <STO> A; Residues: 1-106 <STO> A; Residues: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04559.1; GSPDB:G A; Experimental source: strain C-125 (Senetics: C)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues: 1-335 GBL.
A; Cross-references: GB:J04142; NID:g619799; PIDN:AAA59673.1; PID:g619800
A; Cross-references: GB:J04142; NID:g619799; PIDN:AAA59673.1; PID:g619800
B; Martin, L.H.; Calabi, F.; Milstein, C.
B; Martin, L.H.; Calabi, F.; Milstein, C.
B; Martin, C. Natl.
A; Acternor number: 159088; MUID:87067468; PMID:3097645
A; Reference number: 159088; MUID:87067468; PMID:3097645
A; Status: translated from GB/EMBL/DDBJ
A;Gene: CESP:F14F11.1
A;Map position: 2
A;Introns: 67/1; 93/3; 129/3; 169/3; 201/1; 248/3; 291/1; 325/3; 372/2; 440/3; 499/2;
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14;
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Pred. No. 4
                                                                                                                                                    34.3%; Score 35; 33.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                       255 CPSFHKFVRSPLTIIDVISTGAFF 278
                                                                                                                                                                                                                                                                                                    2 CLSIXRFXXSXXTFIXIXXXMXFF 25
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A;Introns: 71/1
C;Superfamily: osmotic growth protein 1; 3-oxosteroid 1-dehydrogenase homology; fumar
E;40-330/Domain: fumarate reductase flavoprotein homology <FRF>
E;384-487/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>
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A; Residues: 1-670 <LAN>
A; Cross-references: EMBL:AF068718; PIDN:AAC17769.1; GSPDB:GN00023; CESP:R01B10.5
A; Experimental source: strain Bristol N2; clone R01B10
C; Genetics:
A; Gene: CESP:R01B10.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein R01B10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                             Gaps
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A;Introns: 30/2; 70/3; 131/3; 181/3; 275/2; 382/2; 430/2; 455/2; 508
C;Superfamily: Caenorhabditis elegans hypothetical protein R01B10.5
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A;Introns: 11/3; 143/1; 198/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F32H5.6
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Pred. No. 35;
); Mismatches 9; Indels
                                                                                                                                                                                                                                           Length 513;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
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                                                                                                                                                                                                                                     Score 33; DB 2;
Pred. No. 28;
2; Mismatches 1!
A; Experimental source: strain 972h-; cosmid c17A2
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R:Thomas, K.
submitted to the EMBL Data Library, October 1996
A; Reference number: 219308
A; Accession: T20668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.9%; Score 32.5; D
32.3%; Pred. No. 23;
Live 2; Mismatches
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                                                                                                                                                                                                                                     32.4%;
ilarity 32.0%;
Conservative
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Best Local Similarity 32.3
Matches 10; Conservative
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                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                  A; Gene: SPDB:SPAC17A2.05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: CESP: F09F3.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession: T33304
R; Langston, Y.; Bec
                                                                              A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein yibE [imported] - Lactococcus lactis subsp. lactis (strain IL1403) (5/Species: Lactococcus lactis subsp. lactis (5/Species: Lactococcus lactis subsp. lactis (5/Sate: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 (5/Accession: 686725 R:Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlidenome Res. 11, 731-753, 2001 A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss A:Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: Z99292; PIDN: CAB16560.1; GSPDB: GN00066; SPDB: SPAC17A2.05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;302-321/Domain: transmembrane #status predicted <TMM>
F;322-335/Domain: intracellular #status predicted <INT>
F;38.60,126,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;120-184,224-279/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
C;Accession: T37806
R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A;Reference number: 221748
A;Reference number: 221748
                                                                                                                        A;Cross: references: GDB:118764; OMIM:188410
A;Map position: 1922-1923
A;Introns: 21/1; 110/1; 203/1; 296/1; 329/2
A;Introns: 21/1; 110/1; 203/1; 296/1; 329/2
C;Complex: heterodimer with beta-2-microglobulin (see PIR:MGHUB2)
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; thymocyte; transmembrane protein
F;1-19/Domain: slyanal sequence #status predicted <SIG>F;20-335/Product: T-cell surface glycoprotein CDId #status predicted <MAT>F;20-109/Domain: alpha-1 <EX1>
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                                 A:Cross-references: GB:M14664; NID:g180047; PIDN:AAA51935.1; PID:g180048 C;Genetics:
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Pred. No. 19;
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A;Molecule type: DNA
A;Residues: 1-513 <oLL>
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                                                                                                                                                                                                                                                                                                                                                                   F.110-202/Domain: alpha-2 <EX2>
F;203-295/Domain: alpha-3 <EX3>
F;216-281/Domain: immunoglobulin homology <IMM>
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0; Mismatches
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Pred. No.
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26.1%;
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Local Similarity 50.0%;
hes 7; Conservative
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Matches 6; Conserv
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                                                                                                       A; Gene: GDB:CD1D
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Matches
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hypothetical protein yrbD [imported] - Lactococcus lactis subsp. lactis (strain IL140 C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis C; Manager, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001
A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A; Reference number: A6655; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                            A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved seven-pass transmem
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F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:AE005176; PID:g12724677; PIDN:AAK05762.1; GSPDB:GN00146 A;Experimental source: strain IL1403
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C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C;Accession: T14119
R;Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.
Submitted to the EMBL Data Library, October 1997
A;Description: The Celsr family of novel evolutionarily conserved seven-pass A;Reference number: 217881
A;Accession: T14119
A;Accession: T14119
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
                                     A; Accession: E58931
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-492 < ARN>
A; Cross-references: GB:D89861; NID:g4115781; PIDN:BAA36523.1; PID:g4115785
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB 2; Length 492;
Pred. No. 44;
4; Mismatches 11; Indels
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A; Reference number: A58930; MUID: 99030526; PMID: 9801318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
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Pred. No. 46;
0; Mismatches
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C,Superfamily: hypothetical protein sll0855
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Similarity 28.6%;
6; Conservative
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ilarity 57.1%;
Conservative
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A; Molecule type: DNA
A; Residues: 1-512 <STO>
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Matches 8; Conserv
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Best Local S
Matches 6
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T14119
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A;Residues: 1-297 <AND>
A;Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15125.1; PID:e134296
Genetimental source: strain Madrid E
C;Genetics:
A;Gene: RP688
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C;Species: mitcohondrion Cyanidioschyzon merolae
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 03-Jun-2002
C;Accession: E58931
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                                                                                                                                                                                                                                                                             hypothetical protein RP688 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Dates: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: C71675
R;Andersson, S.G.E.; Zomcrodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893 A;Sterence number: A71675 A;Status: preliminary; nucleic acid sequence not shown: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D89865
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (May A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, R.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Accession: D89865
A; Accession: D89865
A; Status: preliminary
A; Molecule type: DNA
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A:Experimental source: strain N315
C;Genetics:
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35;
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                                                                                                          99 CMSINRFIAIYFPFSTI-SKKPFFTNFGIFI 128
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Best Local Similarity 38.95
Matches 7; Conservative
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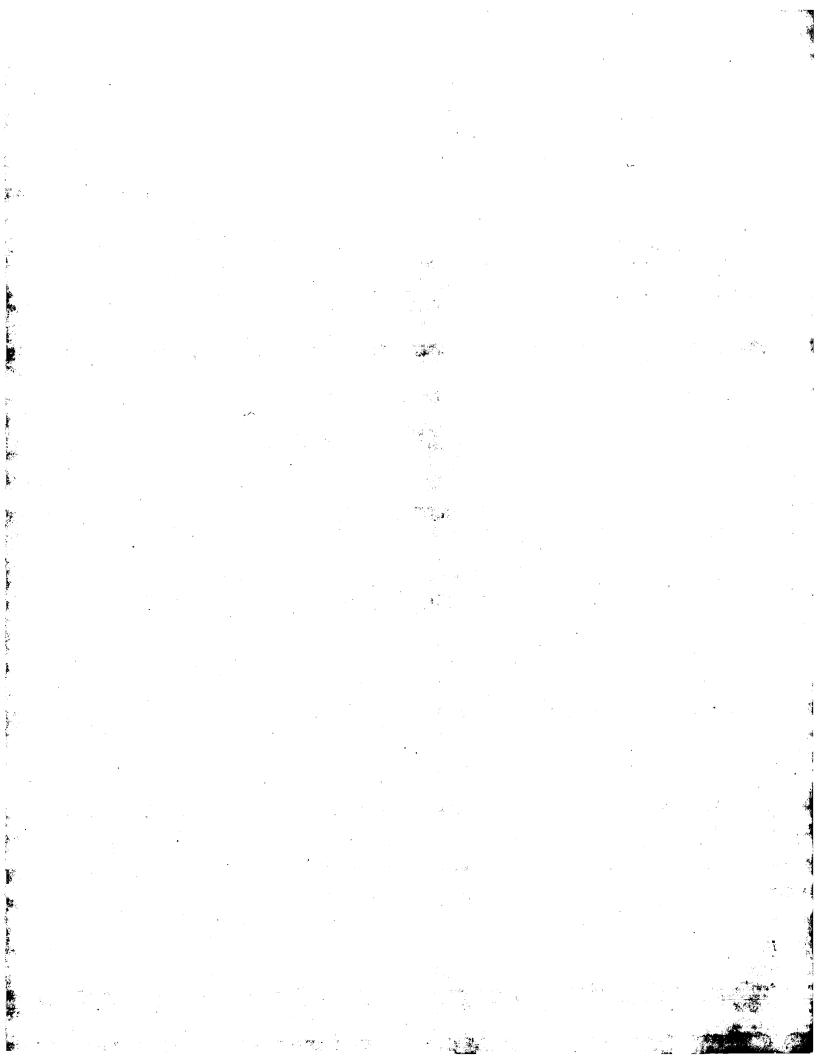
0; Gaps Best Local Similarity 45.5%; Pred. No. 2.1e+02; Matches 5; Conservative 3; Mismatches 3; Indels δ

0

1 RCLSIXRFXXS 11 :|:|: || | 1332 RCVSVLRFDSS 1342

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Search completed: July 16, 2003, 18:09:54 Job time : 6.7774 secs



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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:37:24 ; Search time 1.8887 Seconds (without alignments) 702.728 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-853-079-36 102 1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		di			SUMMARIES	
Result No.	Score	Query	Length	DB	ΩI	न्म
	36	5	376	7	FLH	083710 treponema p
7	35	34.3	2144	Н	CLR2_RAT	2
e	35	4.	2920	Н	CLR2_MOUSE	_
4	35	4.	2923	7	CLR2_HUMAN	Q9hcu4 homo sapien
S	33	32.4	332	Н	CD1D_HUMAN	homo
9	32	31.4	297	7	Y688_RICPR	5 ricke
7	32	31.4	3014	Н	CLR1_HUMAN	9
80	32	31.4		Н	CLR1_MOUSE	mus m
6	32	-		Н	CLR3_MOUSE	snw
10	32	$\overline{}$		Н	CLR3_HUMAN	homo
11	32	31.4	3313	Н	CLR3_RAT	088278 rattus norv
12	31	30.4	361	Н	EBI2_HUMAN	
13	30	29.4	93	-	UBIL_NPVOP	Q05120 orqyia pseu
14	30	29.4	177	-	RM05_ACACA	acantha
15	30	29.4	220	٢	TIM2_CHICK	_
16	30	29.4	330	-	CPDP_VIBFI	vibrio
17	30	29.4	523	٦	YQE4_CAEEL	_
18	30	29.4	549	٦	X92_TRYBB	P12304 trypanosoma
19	30	Ö٦.		٦	YR71_CAEEL	_
20	30	9		٦	XXNX_CLOTM	P38535 clostridium
21	30	on.		Н	KPC1_NEUCR	P87253 neurospora
22	m .	о О	1640	-	CO3_ONCMY	•
23	29.5	28.9	213	-	YK15_YEAST	-
24	6	œ	648	-	RAD4_SCHPO	P32372 schizosacch
25	29	æ	229	-	ABME_RAT	P38483 rattus norv
26	29	8	363	П	VP43_NPVAC	P34050 autographa
27	29	œ	395	Н	ADMR_MOUSE	_
28	29	œ	395	Н		~
29	29	œ		Н	Y294_MYCGE	Q49411 mycoplasma
30	29	∞ .		Н	NU4M_CHOCR	
31	29		49	Н	ADRO_SALFO	P82861 salvelinus
32	29	28.4	569	H	ICS1_ARATH	9s7h
33	29		ŝ	Н	YMM1_CAEEL	4489

	028790 archaeoglob P03783 bacteriopha P47184 saccharomyc			
Y14A_MYCGE OAH3_HUMAN	YE82_ARCFU V42_BPT7 YJ9V_YEAST	V105_FOWPV AG2T_RAT OS25_PLAGA	ABME_MOUSE ABME_RABIT P2Y5_CHICK	NU1M_MYXGL
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137 316	85 112 120	148 177 215	229 236 308	318
27.9	27.5 27.5 27.5	27.5 27.5 27.5	27.5 27.5 27.5	27.5
28.5	7 7 8 8 8 7 8 8 8	7 7 8 8 8 7 8 8	78 78 78 78	28
34 35	36 37 38	39 40 41	44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	45

ALIGNMENTS

· · · · · · · · · · · · · · · · · · ·	RESULT 1 FLHE_TREPA STANDARD; PRT; 376 AA. AC 083710:			RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., A. Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,			(C -!- SIMILARITY: BELONGS TO THE FLHB/HRPN/YSCU/SPAS FAMILY.	This SWISS-PROT entry is copyright. It is between the Swiss Institute of Bioinforthe European Bioinformatics Institute. use by non-profit institutions as lon modified and this statement is not removentites requires a license agreement (sor send an email to license@isb-sib.ch).	CC DR EMBL; AE001244; AAC65681.1; DR TICR; TP0715; DR InterPro; IPR002066; Bac_export_2. DR PEAM; PP01312; Bac_export_2; 1. DR PEANTS; PR00950; TYPE31MSPROT.		Query Match 35.3%; Score 36; DB 1; Length 376; Best Local Similarity 25.8%; Pred. No. 2.3;
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CLR2_RAT RESULT

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PROSITE; PS50221 GPS.
PROSITE; PS50221 GPS.
PROSITE; PS500221 GPS.
PROSITE; PS000222 EGF_1; 6.
PROSITE; PS000229 EGF_1; 6.
PROSITE; PS00049; G_PROTEIN_RECEP_F2_1; FALSE_NEG.
PROSITE; PS00649; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50241; G_PROTEIN_RECEP_F2_4; 1.
G-PROTEIC; PS01248; LAMININ_TYPE_EGF; 1.
G-PROTEIC; Calcium-binding; Laminin EGF-like domain; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CADHERIN 3.
CADHERIN 4.
CADHERIN 4.
EGF-LIKE 1, CALCIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 1.
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EGE-LIKE 7, CALCIUM-BINDING.
EGE-LIKE 8, CALCIUM-BINDING.
EN SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                        4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
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SMART; SM00112; CA; 3,
SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_11ke; 6.
SMART; SM00303; GPS; 1.
SMART; SM00208; HOTEN; 1.
SMART; SM00282; LamG; 2.
PROSITE; PS002010; ASX_HYDROXYL; 2.
PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_1; 3.
                                                                                                                                                                                                                                                                                  Developmental protein;
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                                                                                                      PS50268; 0 PS50221; 0 PS50025; 1
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      Gaps
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-Sprague-Dawley; TISSUE-Brain;
MEDLINE-983800089; PubMed-9693030;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple
EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Cadherin EGF LAG seven-pass G-type receptor 2 (Multiple epidermal growth factor-like domains 3) (Fragment).
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     19; Indels
                                                     CIGVLRFFFTRATTASIONTGWFFVFVRYFM 105
                           2 CLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
     4; Mismatches
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InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF00002; cadhor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EGF_2.
EGF_Ca.
EGF_II.
GPCR_secretin.
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IPR002126; Cadherin.
IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AB011529; BAA88687.1; -. HSSP; P00740; 1EDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00054; laminin_G; l. PRINTS; PR00205; CADHERIN. PRINTS; PR00010; EGFBLOOD. PRINTS; PR00011; EGFLAMININ PRINTS; PR00249; GPCRSECRETIN.
   Conservative
                                                                                                                                                                                                                    Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR001881;
  8;
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                                                                                                                 CLR2_RAT
  Matches
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                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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BGF_2; 2.
BGF_2; 2.
GPROTEIN_RECEP_F2_1; F1
G_PROTEIN_RECEP_F2_2; F1
G_PROTEIN_RECEP_F2_3; 1
G_PROTEIN_RECEP_F2_4; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001879; hormn_receptor.
InterPro; IPR002049; Laminin_GF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR000203; PKD_cys_rich.
Pfam; PF00002; Ttm_2; 1.
Pfam; PF00028; cadherin; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000742; EGF_2.
InterPro; IPR000832; GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00282; LamG; 2.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00232; CADHERIN 1; 6.
PROSITE; PS50268; CADHERIN_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB028499; BAA84070.1; -. EMBL; AF031573; AAC68837.1; -. EMBL; BC005499; AAH05499.1; -.
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9; GPCRSECRETIN.
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SWART; SM0180; EGF_Lam; 1.
SWART; SM00001; EGF_Like; 6.
SWART; SM00303; GPS; 1.
SWART; SM0008; HOTMR; 1.
SWART; SM00282; LamG; 2.
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PRINTS; PR00205; CADHERIN.
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PS50227;
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      ö
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                                                                                                                                                                                                                                                                                   Gaps
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09R0M0; 0922R4; 099K26;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Flamingo 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.; "Developmental expression profiles of Celsr (Flamingo) genes in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mech. Dev. 112:157-160(2002). 
 -!- FUNCTION: Receptor that may have an important role in cell/cell
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                            DB 1; Length 2144;
  BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases
                                                                    N.LINKED GECNAC...)
                                                                                                                                                                                                                 (GLCNAC
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Pred. No. 21;
2; Mismatches
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MEDLINE-99418630; PubMed=10490098;
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54.5%;
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                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PubMed=10790539;
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CELSR2.
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[2]
SEQUENCE OF 516-2923 FROM N.A.
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54.5%;
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1243 RCVSVLRFDSS 1253
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PROSITE; PS50025; LAM G_DOMAIN; 2. G-protein coupled receptor; Transmembrane; Glycoprotein; EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat; Developmental protein; Hydroxylation; Signal.
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                                                                                      CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 2.
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EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 1.

EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
EGF-LIKE 9, CALCIUM-BINDING.
EGF-LIK
                                                                                                                                                                                                                                                                                                                                                                                                                             CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
CADHERIN 6.
CADHERIN 8.
CADHERIN 9.
CADHERIN 9.
CAGHERIN 9.
CAGHER
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7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CADHERIN 1.
CADHERIN 2.
                                                                                                                                                                         2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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| PT CARBONIND 1556 1566 N-LINERD GLOAMC. ) [POTENTIAL].
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Gaps
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Pred. No. 28;
;; Mismatches 3; Indels
CADHERIN 8.

CADHERIN 9.

CADHERIN 9.

CGF-LIKE 1, CALCIUM-BINDING.

EGF-LIKE 2, CALCIUM-BINDING.

LAMININ G-LIKE 1.

EGF-LIKE 6, CALCIUM-BINDING.

EGF-LIKE 6, CALCIUM-BINDING.

EGF-LIKE 7, CALCIUM-BINDING.

EGF-LIKE 7, CALCIUM-BINDING.

EGF-LIKE 8, CALCIUM-BINDING.

EGF-LIKE 10.

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ID CDID_HUMAN STANDARD;
AC P15813; Q9Y5M4;
DT 01-APR-1990 (Rel. 14, Created)
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54.5%;
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                                                                                   CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 2.
EXTRACELLULAR (POTENTIAL).
I (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
7 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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CADHERIN 2.
CADHERIN 3.
CADHERIN 4.
CADHERIN 5.
CADHERIN 6.
  or send an email to license@isb-sib.ch)
                       EMBL; AF234887; AAG00080.1; -
EMBL; D87469; BAA13407.1; -
HSSP; P15116; 1NCJ.
Genew; HGNC:3231; CELSR2.
MIN; 604265; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 19-109 FROM N.A., AND VARIANT SER-64.

MEDLINE-99416841; Pubmed=10488738;
A Hann M., Hannick L.I., Dibrino M., Robinson M.A.;
Then M., Hannick L.I., Dibrino M., Robinson M.A.;
Tissue Antigens 54:122-127(1999).
Tissue Antigens 54:122-127(1999).
TISSUE ANTIGORIAN NOT KNOWN.
TISSUE SPECIFICITY: EXPRESSED ON CORTICAL THYMOCYTES, ON CERTAIN
TISSUE SPECIFICITY: BELONGS TO THE IMMUNOCLOBULIN SUPERFAMILY.

THE THYMOCYTES TO THYMOCYTES 
                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
T-cell surface glycoprotein CDld precursor (CDld antigen) (R3G1).
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BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                      Balk S.P., Bleicher P.A., Terhorst C.; "Isolation and characterization of a cDNA and gene coding for Fourth CDI molecule", "Isolath CDI molecule", Proc. Natl. Acad. Sci. U.S.A. 86:252-256(1989).
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SMART; SM00407; IGc1; 1.
Glycoprotein; Signal; Transmembrane; Immunoglobulin domain;
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BY SIMILARITY.
BY SIMILARITY.
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Calabl; F., Jarvis J.W., Martin L., Milstein C.;
"Two classes of CDI genes.":
Eur. J. Immunol. 19:285-292(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, L38820, AAA59672.1; --
EMBL, L38815, AAA59672.1; JOINED.
EMBL, L38815, AAA59672.1; JOINED.
EMBL, L38816, AAA59672.1; JOINED.
EMBL, L38818; AAA59672.1; JOINED.
EMBL, L38819, AAA59672.1; JOINED.
EMBL, L38819, AAA59672.1; JOINED.
EMBL, J04142, AAA59673.1; --
                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. 'MEDLINE=89098892; PubMed=2463622;
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InterPro; IPR003597; Ig_c1.
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                                                                                Homo sapiens (Human)
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PIR; A32217; A32217
                                                                                                                                                                              SEQUENCE FROM N.A.
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Science 290:347-350(2000).
-!- SIMILARITY: STRONG, TO R.PROWAZEKII RP689. SOME TO H.INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Madrid E;
MEDLINE-299139499; PubMed-9823893;
Andersson J.O.,
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eliksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of mitochondria."
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
T -> S.
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Ogata H., Audic S., Barbe V., Artiguenave F., Fournier P.-E.
Raoult D., Claverie J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=782;
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                                                                                                                                                      Length 335;
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TIGREAMs; TIGR01045; RPE; 1.
Hypothetical protein; Transmembrane; Complete proteome.
                                                                         /FTId=VAR_010211.
EA041C1C45A5777F CRC64;
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                                                                                                                                                      Score 33; DB 1;
Pred. No. 9.2;
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Last annotation update)
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16-0CT-2001 (Rel. 40, Last sequal 16-0CT-2001 (Rel. 40, Last annowny Hypothetical protein RP688.
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                                                                                                     37717 MW;
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50.0%;
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Best Local Similarity 50.0.
The Conservative Transfer Conservative ....
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297 AA;
                                                                                                       335 AA;
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les 7; Conserv
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REDINING_20057165; Pubbmed=10591208;
RA Dunham I. Hunt A.R., Collins B. Bruskiewich R., Beare D.M., Clamp M., Smitk L.J., Almacough R., Almeida J.P., Babbage A.K., Radauley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Radauley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Bagguley C., Bailey J., Barlow K.F., Carter N.P., Chen Y., Clark G., Burklil W.D., Burton J., Carder C., Carter N.P., Chen Y. Clark G., Burklil W.D., Burton J., Carder C., Carter N.P., Chen Y. Clark G., Conroy D., Corby N.R., Colleg S.M., Fleming K., French L., Garner A.A., G. R., Goward M.F., Grahman D.V., Griffiths M.N.D., Hall C., Radiner J.G.R., Goward M.E., Grahman D.V., Griffiths M.N.D., Hall C., Radiner J.G.R., Langford C.F., Carershaw J., Klunberley A.M., King A., Hunt S.E., Jones M.C., Kershaw J., Klunberley A.M., Mashrechii-Mohammadi M., Matthews L.H., Mccaun O.T., Marity G., Hearloott R.M., Mashrechii-Mohammadi M., Matthews L.H., Mccaun O.T., Marity G., Hearloott R.W., Mashrechii-Mohammadi M., Matthews L.H., Mccaun O.T., Marity G., Hearloott R.W., Mashrechii-Mohammadi M., Matthews L.H., Mccaun O.T., Mallings S.H., Plumb R.W., Stewersha M., Stewersha M., Stewersha M., Stewersha M., Steward C.B., Sahra H.K., Stewer C.D., Sanalley S., Smith M. L., Soderlund C., Spragon L., Steward C.B., Sulaton J.E., Swann R.M., Milliamson H., Williams S., Rawsaki K., Sasaki T., Asakawa S., Kudoh J., Radina S., Rawsaki K., Sasaki T., Asakawa S., Kudoh J., Rangan B., Mulliams S., Rawsaki K., Sasaki T., Asakawa S., Kudoh J., Rhintan A., Shibuya K., Woshizaki Y., Asakawa S., Kudoh J., Rhintan A., Shibuya K., Woshizaki Y., Asakawa S., Kudoh J., Rhintan A., Shibuya K., Woshizaki Y., Moll. M., Millson R., Mang Y., Mang Y., Mang Y., Mul R., Mang Y., Mang Y., Wang Z., White J., Williamson D., Brahley D., Bradenban H., Bulton R., Johnson D., Bemis G., Bertley D., Bradenban H., Shintan R., Shaikh T., Kurahashi H., Saitta S., Balan M., Shongu H., Shinuya H., Shongu H., Shinuya H., Shongu H., Shinuya H., Shongu H., Shinuya H., Shongu H., Shinuya H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Strausberg R.; Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. -:- FUNCTION: Receptor that may have an important role in cell/cell
                         CLR1_HUMAN STANDARD; PRT; 3014 AA.
09NYO6; Q9Y526; Q9Y506; O95722; Q9BWQ5;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo
                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                         'Large exons encoding multiple ectodomains are a characteristic
                                                                                                                                                                                                                                                                        feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 624-3014 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=20202599; Pubmed=10716726;
Wu Q., Maniatis T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402:489-495(1999).
                                                                                                               homolog 2) (hFmi2).
CELSR1 OR CDHF9 OR FMI2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'The DNA sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tilahun Y., Wright
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'ISSUE=Kidney;
               CLR1_HUMAN
RESULT
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                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                      -!- SÜBCELLÜLAR LOCATION: Integral membrane protein.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be produced by alternative splicing.
-!- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
-!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ GG-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 1.
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2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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nervous system formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G_PROTEIN_RECEP_F2_1;
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EMBL, AL031588; CAB38413.1; -.
EMBL, BC000059; AAH00059.1; -.
Genew, HGNC:1850; CELSRI.
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Laminin_EGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001791; Laminin_G.
InterPro; IPR000203; PKD_cys_rich.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF00028; cadherin; 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF231024; AAF61930.1; -. EMBL; AL021392; CAB50707.1; -.
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PRINTS, PR00205; CADHERIN.
PRINTS; PR00211; EGFLAMININ.
PRINTS; PR00249; GPCRSECRETIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00249; GPCRSECRETIN SMART; SMO0112, CA; 9.
SMART; SM00180; EGF_LAM; 1.
SMART; SM00001; EGF_like; 6.
SMART; SM00303; GPS; 1.
SMART; SM00008; HOTMR; 1.
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PROSITE; PS01186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kidney and epithelia.
--- TISSUE SPECIFICITY: Expressed in the brain, where it is localized principally in the ependymal cell layer, choroid plexus and the area postrema. Also found in spinal chord and in the eye.
--- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
--- SIMILARITY: CONTAINS 9 CADHERIN DOWAINS.
--- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOWAINS.
--- SIMILARITY: CONTAINS 1 LAMININ GF-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                    Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.; "Developmental expression profiles of Celsr (Flamingo) genes in the mouse.";
                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                   Hadjantonakis A.-K., Formstone C.J., Little P.F.R.;
"mcelsr1 is an evolutionarily conserved seven-pass transmembrane
receptor and is expressed during mouse embryonic development.";
Mech. Dev. 78:91-95(1998).
                                                                                                                                                                    STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=97480720; PubMed=9339365; Hadjantonakis A.-K., Sheward W.J., Harmar A.J., de Galan L., Hoovers J.M. N., Little P.F.R.; "Celsr1, a neural-specific gene encoding an unusual seven-pass transmembrane receptor, maps to mouse chromosome 15 and human chromosome 22gter." Genomics 45:97-104(1997).
   Cadherin EGF LAG seven-pass G-type receptor 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch)
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Laminin_EGF.
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GPCR_secretin.
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InterPro; IPR002126; Cadherin.
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                         Mus musculus (Mouse).
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InterPro; IPR000832;
InterPro; IPR001879;
                                                                                                                                                                                                                                                             [3]DEVELOPMENTAL STAGE.
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InterPro; IPR001791;
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HSSP; P00749; 1URK.
                                                                              SEQUENCE FROM N.A.
                                                                                                                                                          TISSUE SPECIFICITY
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CADHERIN 6.
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CALIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
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EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
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3; Indels
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CYTOPLASMIC (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
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EGF-LIKE 4, CALCI
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CLR3_MOUSE STANDARD; PRT; 3301 AA.

15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 3 precursor.

CELSR3.

Mus musculus (Mouse).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentla; Sciurognathi; Muridae; Murinae; Mus.

CLR3_TAXID=10090;
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R PROSITE; PS01022; EGF_1; 6.
R PROSITE; PS01221; EGF_2; 2.
R PROSITE; PS01221; GPS 1.
R PROSITE; PS0124; GPROTEIN_RECEP_F2_1; FALSE_NEG.
R PROSITE; PS00649; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
R PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
R PROSITE; PS50201; G_PROTEIN_RECEP_F2_4; 1.
R PROSITE; PS005025; LAMININ_TYPE_EGF; 1.
R PROSITE; PS0025; LAMIN_TYPE_EGF; 1.
R PROSITE; PROSITE; PROSITE; LAMIN_TYPE_EGF; 1.
R PROSITE; PS0025; LAMIN_TYPE
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CADHERIN EGF LAG SEVEN-PASS G-TYPE
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InterPro; IPR000203; PKD_cys_rich. Pfam; PF00028; cadherin; 9. Pfam; PF00008; EGF; 6. Pfam; PF00008; EGF; 6. Pfam; PF001825; GPS; 1. Pfam; PF001825; GPS; 1. Pfam; PF00053; laminin_EGF; 1. Pfam; PF00054; laminin_EGF; 1. PRINTS; PR000154; laminin_G; 1. PRINTS; PR000155; CADHERIN. PRINTS; PR00112; CAPERAMININ. PRINTS; PR00112; CAPERAMININ. PRINTS; PR00112; CAPERAMININ. PRINTS; PR00112; CAPERAMININ. PRINTS; SN00100; EGF_Lam; 1. SMART; SN00100; EGF_Lam; 1. SMART; SN00008; Lamic; 2. PROSITE; PS00010; ASX_HYDROXYL; 2. 9. PROSITE; PS
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DORAN TELLITITE ELITITE ELITIT

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PROSITE; PS01248; LAWIN_TYPE_EGF; 1.

PROSITE; PS50221; GPS; 1.

PROSITE; PS50221; GPS; 1.

PROSITE; PS50629; G_PROTEIN_RECEP_F2_1; FALSE_NEG.

PROSITE; PS00640; G_PROTEIN_RECEP_F2_2; FALSE_NEG.

PROSITE; PS50227; G_PROTEIN_RECEP_F2_2; FALSE_NEG.

PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.

G-protein coupled receptor; Transmembrane; Glycoprotein;

EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;

Developmental protein; Hydroxylation; Signal.
                                                                                                                                            CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 3.
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EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 2.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
LAMININ EGF-LIKE.
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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             EGF_1; 5.
EGF_2; 4.
LAMININ_TYPE_EGF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CADHERIN_2; 8
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             PS00022;
PS01186;
    PS50268;
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                               Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.; "Developmental expression profiles of Celsr (Flamingo) genes in the
                                                                                                    Formstone C.J., Little P.F.R.; The flamingo-related mouse Celsr family (Celsrl-3) genes exhibit distinct patterns of expression during embryonic development."; Mech. Dev. 109:91-94(2001).
                                                                                 SEQUENCE OF 2574-3046 FROM N.A., AND DEVELOPMENTAL STAGE. Pubmed=11677057;
SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGES.
STRAIN-C57BL/6;
Pubmed-11850187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF127498; AAL25099.1; --
EMBL; AF188752; AAG17057.1; ALT_FRAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IPR001879; hormn_receptor IPR002049; Laminin_EGF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR002126; Cadherin.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPRO01791; Laminin_G.
InterPro; IPRO00203; PKD_cys_rich.
Pfam; PF00002; 7tm_2; 1.
                                                    mouse.";
Mech. Dev. 112:157-160(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00054; laminin_G; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000742; EGF_2.
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Pfam; PF00008; EGF; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1858236; Celsr3.
                                                                                                                                                      TISSUE SPECIFICITY.
PubMed=10790539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF01825;
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Pfam;

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3312
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-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-i- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
-i- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLR3_HUMAN STANDARD, PRT; 3312 AA.

CD80YQ7; 075092;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Created)
16
                                                                       N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20202599; PubMed-10716726;
Wu Q., Maniatis T.;
"Large exons encoding multiple ectodomains are a characteristic
                                                                                                                                                                                                                                                                                                 (POTENTIAL)
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Pred. No. 1.4e+02;
3; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                              R -> P (IN REF. 2).
MW; A6B18F2DF7F4DEB6 CRC64;
                                                             HYDROXYLATION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC.
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MEDLINE-98360089; PubMed-9693030;
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45.5%;
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Best Local Similarity 45...
5; Conservative
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838
11173
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21185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G-protein coupled receptor; Transmembrane; Glycoprotein;
EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
Developmental protein; Hydroxylation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
CADHERIN EGF LAG SEVEN-PASS G-TYPE
RECEPTOR 3.
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1 (POTENTIAL).
2 (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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5 (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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FALSE_NEG.
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PROSITE; PS00010, ASX_HYDROXYL; 1.

PROSITE; PS00010, ASX_HYDROXYL; 1.

PROSITE; PS00023; CADHERIN_1; 7.

PROSITE; PS00022; EGF_1; 6.

PROSITE; PS01186; EGF_2; 4.

PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; FALSE_PROSITE; PS00649; G_PROTEIN_RECEP_F2_2; FALSE_PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_PROSITE; PS00650; G_PROTEIN_RECEP_F2_3; 1.

PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.

PROSITE; PS00489; LAM_LODMAIN, 2.

PROSITE; PS01248; LAM_LODMAIN, 2.
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CYTOPLASMIC (1
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InterPro; IRR000126; Cadherin.
InterPro; IRR000561; EGF-1ike.
InterPro; IRR000181; EGF_Ca.
InterPro; IRR001879; horm_receptor.
InterPro; IRR001879; horm_receptor.
InterPro; IRR001879; Laminin_EGF.
InterPro; IRR001879; Laminin_Gr.
InterPro; IRR001879; Laminin_Gr.
InterPro; IRR000203; PKD_cys_rich.
Pfam; PF000028; cadherin; 9.
Pfam; PF000028; EGF; 6.
Pfam; PF00008; EGF; 6.
Pfam; PF00008; IGF; 6.
Pfam; PF00008; IGF; 6.
Pfam; PF00008; IGF; 1.
Pfam; PF00008; IMM; 1.
                                                                                                                                                                                                                                                                                MIM; 604264; -. InterPro; IPR000152; Asx_hydroxyl
                                                                                                                                                                                     EMBL; AF231023; AAF61929.1; -. EMBL; AB011536; BAA32464.1; -.
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PRINTS; PR00249; GPCRSECRETIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART; SM00112; CA; 8.
SMART; SM001180; EGF_Lam; 1.
SMART; SM00001; EGF_like; 6.
SMART; SM00303; GFS; 1.
SMART; SM0008; HOTMR; 1.
SMART; SM00282; LamG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00205; CADHERIN.
                                                                                                                                                                                                                                                             Genew; HGNC: 3230; CELSR3.
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                                          15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel.)
16-JUN-2002 (Rel.)
17-JUN-2002 (Rel.)
18-JUN-2003 (Rel.)
18-
                                                                                                                                                                                                                                                                                                                                                brain stem.

-! SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: COWTAINS 9 CADHERIN DOMAINS.
-!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
3313 AA
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InterPro; IPR0010525, Asx_hydroxyl.
InterPro; IPR001026; Cadherin.
InterPro; IPR001026; Cadherin.
InterPro; IPR000742; EGF_2.
InterPro; IPR000181; EGF_Ca.
InterPro; IPR001081; DGF_Ca.
InterPro; IPR001087; horm_receptor.
InterPro; IPR001097; Laminin_EGF.
InterPro; IPR001097; Laminin_EGF.
InterPro; IPR001097; Laminin_GF.
InterPro; IPR001097; PRD_Cys_rich.
Ffam; PF00008; EGF; F.
Ffam; PF00008; EGF; F.
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SMART; SM00180; EGF_Lam; 1.
SMART; SM00001; EGF_Like; 6.
SMART; SM00303; GPS; 1.
SMART; SM00208; HormR; 1.
SMART; SM00282; LamG; 2.
PROSITE; PS00100; ASX_HYDROXYL; 1.
PROSITE; PS00232; CADHERIN 1; 7.
PROSITE; PS50268; CADHERIN 1; 7.
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PS01186; EGF_2; 4.
PS50221; GPS; 1.
PS50025; LAM_G_DOMAIN;
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Pfam; PF02793; HRM; 1.
Pfam; PF00054; laminin_G; 1.
PRINTS; PR00205; CADHERIN.
  STANDARD;
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                                       CADHERIN G.
EGF-LIKE J. CALCIUM-BINDING.
EGF-LIKE J. CALCIUM-BINDING.
EGF-LIKE S. CALCIUM-BINDING.
EGF-LIKE J. CALCIUM-BINDING.
EGF-LIKE J
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Pred. No. 1.4e+02;
3; Mismatches 3; Indels
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MW; BEC208703651A4A5 CRC64;
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1389 KCVSVLRFDSS 1399
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-93180173; PubMed-8383238;
Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
Kieff E.;
"Epstein-Barr virus-induced genes: first lymphocyte-specific G
protein-coupled peptide receptors.";
J. Virol. 67:2209-2220(1997).
FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS ON B
LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
INDUCTION: BY EBV.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
                                                                                                                                                                                                                                                                                        Gaps
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Catarrhini; Hominidae; Homo.
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Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
STOROTEIN COUPLED TO SETTRACELLULAR (POTENTIAL).
TRANSMEM 32 57 1 (POTENTIAL).
                                                                                                                                                                                                                           CRC64;
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                                                                                                                                                                                                                                                       Score 32; DB 1; Le
Pred. No. 1.4e+02;
3; Mismatches 3;
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15-JUN-2002 (Rel. 41, Last annotation update)
EBV-induced G protein-coupled receptor 2 (EBI2)
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01-OCT-1993 (Rel. 27, Last seq
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Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                        31.48;
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1380 KCVSVLRFDSS 1390
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MIM; 605741; -.
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tes 5; Conserv
              NCBL_TaxID=9606;
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Matches
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             PROSITE; PSO0650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS50221; G_RROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_RROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
EGF101; Coupled receptor; Transmembrane; Glycoprotein; EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat; Developmental protein; Hydroxylation; Signal.
                                                                                                                                           CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 3.
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CACIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 1.
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EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
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EXTRACELULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL).
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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177 AA

Matches

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RESULT 13

DB 1; Length 93,

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STRAIN=ATCC 30010 / NEFF;

MEDLINE-95147275; PubMed-7844823;

Burger G., Plante I., Lonergan K.M., Gray M.W.;

The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba castellanii: complete sequence, gene content and genome organization."

J. Mol. 18101. 245:522-537(1995).

SUBCELLULAR LOCATION: Mitochondrial.

SIMILARITY: BELONGS TO THE LSP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                            MULTIUBIQUITIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS.
681B2A99DE964C99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%; Score 30; DB 1; Length 177; 37.5%; Pred. No. 22;
                                                                                                       NECESSARY FOR BRANCHED-CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NoV-1995 (Rel. 32, Created)
01-NoV-1995 (Rel. 32, Last sequence update)
01-NOV-2000 (Rel. 39, Last annotation update)
Mitochondrial 60S ribosomal protein L5.
                                                                                                                                                                                                                                                       2; Mismatches
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Pfam; PF00281; Ribosomal_L5; 1.
PROSITE; PS00358; RIBOSOMAL_L5; FALSE_NEG.
Ribosomal protein; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID=5755;
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Pred. No.
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PRINTS; PR00348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
                                                                                      Nuclear protein; Late protein.
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                                                                                                                                                                     93 AA; 10427 MW;
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85 RCLSLLQF 92
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RM05_ACACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-93286576; PubMed-8389803; Russell R.L.O., Rohrmann G.F.; "Nucleotide sequence of the ubiquitin-39K gene region from the Orgyla pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; J. Gen. Virol. 74:1191-1195(1993).
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Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
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INTERACTION WITH G PROTEINS.
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                     2 (POTENTIAL)
EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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  CYTOPLASMIC (POTENTIAL).
                                                              3 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
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01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Ubiquitin-like protein.
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EMBL; U75930; AAC59024.1; -.
PIR; J02029; J02029.
HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                                                                                                                                                                 41224 MW;
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361 AA;
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MEDLINE-98122528; PubMed-9462696;
MEDLINE-98122528; PubMed-9462696;
Mines R.T., Li L.H., Weaver B., Hawkes S., Hahn-Dantona E.A.,
Quigley J.P.;
"Cloning, expression, and characterization of chicken tissue
inhibitor of metalloproteinase-2 (TIMP-2) in normal and transformed
chicken embryof ilbroblasts.",
J. Cell. Physiol. 174:342-352(1998).
I- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES)
AND IRREVERSIBLY INACTIVATES THEM (BY SIMILARITY).
I- SUBCELLULAR LOCATION: Secreted.
I- PTW. THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF
DISULFIDE BONDS.
15-JUL-1998 (Rel. 36, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
metalloproteinases-2).
                                                                                Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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61BDAC760B752E53 CRC64;
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Metalloprotease inhibitor; Signal.
SIGNAL 1 26 BORDEN
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Search completed: July 16, 2003, 17:47:26 Job time : 3.8887 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 16, 2003, 17:37:48 ; Search time 7.77066 Seconds Run on:

(without alignments) 848.513 Million cell updates/sec

US-09-853-079-36 102 1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32 Perfect score:

Sequence:

Scoring table:

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Total number of hits satisfying chosen parameters:

671580 seqs, 206047115 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPTREMBL_21:* Database

sp_archea:* sp_bacteria:*

sp_fungi:*
sp_human:*
sp_nvertebrate:*
sp_mammal:*
sp_mhc:*

sp_organelle:*
sp_phage:*
sp_plant:*
sp_rodent:*

sp_virus:*
sp_vertebrate:*
sp_unclassified:*

sp_rvirus:*
sp_bacteriap:*
sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Q9nim3 babesia mic	Q949u7 arabidopsis	Q91f96 arabidopsis	Q56337 treponema p	Q19464 caenorhabdi	Q9qyp2 rattus norv	Q92566 homo sapien	Q9r0m0 mus musculu	Q9hcu4 homo sapien	Q9kel2 bacillus ha	Q96cl0 homo sapien	Q96ux9 hebeloma cy	Q9vwg4 drosophila	Q9chc5 lactococcus	Q9vwk3 drosophila	013755 schizosacch
SUMMAKIES			ΩI	Q9NIM3	0 094907) Q9LF96	056337	Q19464	l Q9QYP2			Q9HCU4	5 Q9KEL2	Q96CL0	6X0960	Q9VWG4	5 Q9CHC5	Q9VWK3	013755
			Match Length DB	206 5	234 10	234 10	366 2	.776 5	2144 11	2408 4		2923 4	106 16	402 4	492 3	700 5	393 16	481 5	513 3
	dР	Query	Match L	73.5	35.3	35.3	35.3	34.3	34.3	34.3	34.3	34.3	33.3	33.3	33.3	33.3	32.4	32.4	32.4
			Score	75	36	36	36	35	35	35	35	35	34	34	34	34	33	33	33
		Result	No.	-	7	m	4	S	9	7	8	6	10	11	12	13	14	15	16

Q9n976 Leishmania P90821 caenorhabdi Q9tb48 platynereis Q9kz2 thermoplasm Q9y506 homo sapien	099vbl staphylococ Q9rcb5 yersinia ps Q96x22 magnaporthe Q8rmf0 streptococc Q92xq1 cyanidlosch Q9cf17 lactococcus	O9fhyd5 homo sapien Q9fhl8 arabidopsis Q9hed6 neurospora Q9hyd6 homo sapien O35161 mus musculu Q91210 mus musculu	Q9nyq7 homo sapien Q88278 rattus norv Q94213 mus musculu P91256 caenorhabdi Q905a7 schistosoma Q99jv7 mus musculu	Q20416 caenorhabdi Q8hrBo clostridium Q9h6f9 homo sapien Q9d5z1 mus musculu P73992 synechocyst Q67551 garlic late
5 Q9N976 5 P90821 8 Q9TB48 17 Q9HKZ2 1 Q9Y506	16 Q99VB1 2 Q9KCB5 3 Q96K22 2 Q8RMF0 8 Q9ZKQ1 16 Q9CF17	4 Q9BWQ5 10 Q9FHI8 3 Q9HED6 14 Q9NYQ6 11 Q91ZI0		5 Q20416 16 Q8XHEO 4 Q9H6F9 11 Q9D5Z1 16 P73992 12 Q67551
1086 312 308 347 355				173 201 244 260 264 312
32.4 31.9 31.4 31.4	31. 31. 31. 44. 31. 44. 44. 47. 47.	31.44.44.44.44.44.44.44.44.44.44.44.44.44	31.4 31.4 30.9 30.9 30.9	300.8 4.00.8 3.00.8 4.00.8 4.00.8
32 32.5 32 32 32	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	32 31.5 31.5 31.5 31.5	33333
17 18 19 20 21	22 24 25 27	. 28 29 30 32 33	888 37 38 39 39	44444444444444444444444444444444444444

ALIGNMENTS

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STRAIN-MN1;
MEDLINE-2021818; PubMed=10768973;
Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D.,
Benson D.R., Krause P.J., Reed S.G., Persing D.H.;
"Serological expression cloning of novel immunoreactive antigens of
Babesia microti.";
Infect. Immun. 68:2783-2790(2000).
EMBL, AR206526; AAF68254.1; -.
SEQUENCE 206 AA; 24963 MW; 4287DE5D8FD15C94 CRC64;
                                                                                     Babesia microti.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                            Length 206;
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Last'sequence update)
Last annotation update)
                          01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
Seroreactive antigen BMN1-17B.
                                                                                                                                                                                                                                                                                                            73.5%; Score 75; DB 5; 1
53.1%; Pred. No. 7.5e-09;
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206 AA.
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PRT;
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01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                            Query Match 73.5%
Best Local Similarity 53.1%
Matches 17; Conservative
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PRELIMINARY;
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Submitted (JAN-2002) to the EM EMBL; AL132969; CABB6900.1; -- EMBL; AV054678; AAK96829.1; -- EMBL; AY05493; AAL66908.1; --
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Best Local Similarity 25.0v
Local 8; Conservative
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01-JUN-2002 (TEMBLEEL.
FILB'.
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                                                                                                                                                Similarity 7; Conserva
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Best Local S
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                                                                                                                A Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,

RA Goldsmith A.D., Jiang P.K., Lee J.M., Onodera C.S., Quach H.L.,

RA Goldsmith A.D., Jiang P.K., Lee J.M., Onodera C.S., Quach H.L.,

RA Carninci P., Chen H., Yamamura Y., Yu S., Bowser L., Jones T.,

RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,

Lin J., Meyers M.C., Miranda M., Narusaka M., Nquyen M., Palim C.J.,

RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

"Full Length cDNA of gene FeJ2_130/AT3552960 (GI:7529720).";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

REMBL; AKO50880; AAK92817.1;

RICEPRO; IPRO00866; AHQ-TSA.

REMBL; RY050880; AARC-TSA.

REMBL; RY050880; AARC-TSA.

REMBL; RY050880; AARC-TSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOUTBNICE FROM N.A.
SOUTBNICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Soutbwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Chan M., Gawser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Saki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                  Arabidopsis thaliana (Mouse-ear cress).

Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peroxiredoxin-like protein.
F8J2_130 OR AT3G52960, F8J2_130.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,

Nyakatura G., Fartmann B., Mauner D., Sterr W., Holland R.,

Ouetiber B., Salanoubat M.;

Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                         DB 10; Length 234;
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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Pred. No. 4.4;
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   peroxiredoxin protein.
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SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
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                                                                          NCBI_TaxID=3702;
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Gaps
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"Identification and sequences of the Treponema pallidum fliM', fliY, fliP, fliQ, fliR and flhB' genes.";
Gene 166:57-64(1995).
EMBL: U36899; AAB00549.1; -.
InterPro: IPR002066; Bac_export_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                            Length 234;
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to the EMBL/GenBank/DDBJ databases
                                                                                                   InterPro; IPR000866; Ahpc-TSA.
Pfam; PF00578; Ahpc-TSA; 1.
SEQUENCE 234 AA; 24684 MW; 4F66DA63CD15F003 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
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Last annotation update)
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Last sequence update)
Last annotation update)
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Pred. No. 4.4;
2; Mismatches 7
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                                                                                                                                                                                         35.3%;
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Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;
Tenaka A., Kotani H., Miyajima N., Nomura N.;
Prediction of the coding sequences of unidentified human genes. VI.
the coding sequences of 80 new genes (KIAA0201 KIAA0280) deduced by analysis of CDNA clones from cell line KG-1 and brain.";
I- SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
EMBL, D87469; BAA13407.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                               R SMART; SW00179; CA: 3.

R SMART; SW00179; EGF_CA: 1.

R SMART; SW00109; EGF_Like: 6.

SMART; SW000008; HormR: 1.

R SMART; SW00008; HormR: 1.

R SMART; SW00208; TNRR: 1.

R SMART; SW00208; TNRR: 1.

R PROSITE; PS00208; CADHERIN_1; 2.

R PROSITE; PS00222; CADHERIN_1; 2.

R PROSITE; PS00222; CADHERIN_2: 4.

R PROSITE; PS01186; EGF_2: 4. UNKNOWN_6.

R PROSITE; PS01186; EGF_2: 4.

R PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.

R PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UND-2002 (TrEMBLrel. 21, Last annotation update)
KIAA0279 protein (Fragment).
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2; Mismatches
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Laminin_EGF.
Laminin_G.
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EGF_Ca.
EGF_II.
GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; DOTAC: HSSP: P15116; INCJ.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR00126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97191544; PubMed=9039502;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF-like.
                                                                                                                                                                                           GPCRSECRETIN.
                                                                                                     laminin_G; 1.
                                                                                                                                                                         PRINTS; PRO0011; EGFLAMININ.
     cadherin; 3.
                                                                                                                       PRINTS; PR00205; CADHERIN.
                                                                                                                                                     EGFBLOOD
                                   ; PF02793; HRM; 1.
PF00054; laminit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           467 RCVSVLRFDSS 477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                   PR00249;
                                                                                                                                                   PRINTS; PR00010
     PF00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIAA0279.
                                                                                                                                                                                              PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  092566
       Pfam;
                                                     Pfam;
Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 7
Q92566
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       ORRES DE RESERVA DE LA COMBINA DE LA COMBINA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Métazoa; Chórdata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBL_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                     Genome sequence of the nematode C.elegans: A.platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.3%; Score 35; DB 5; Length 776; llarity 33.3%; Pred. No. 21; Conservative 2; Mismatches 14; Indels
                                                                       Lightning J.;
Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87162 MW; 96A83E3FCBD25F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 2144 AA
                                                                                                                                                                                                                                                        LINESTIGATING DIOLOGY;
Science 282:2012-2018(1998).
EMBL; Z54307; CAA91092.1; -.
INTECTPO: IPRO00210; BTB_POZ.
INTECTPO: IPRO0122; K+Channel_pore.
INTECTPO: IPRO01368; K_channel.
INTECTPO: IPRO01391; K_channel.
INTECTPO: IPRO01391; K_tetra.
INTECTPO: IPRO01391; K_tetra.
INTECTPO: IPRO01391; K_tetra.
INTECTPO: IPRO013974; Shaw_channel.
PRAMT: PRO0150; IOn_trans; 2.
Pfam; PF002214; K_tetra: 1.
PRINTS; PR001499; KCHANNEL.
PRINTS; PR001499; KCHANNEL.
PRINTS; PR001499; SHAWCHANNEL.
SMART; SM00225; BTB; 1.
SEQUENCE 776 AA; 87162 MW; 96A83E31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      255 CPSFHKFVRSPLTIIDVISTGAFF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | IPR000742; EGF_2.
| IPR001881; EGF_Ca.
| IPR001488; EGF_III.
| IPR000832; GPCR_Secretin.
| IPR001879; hormn_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CLSIXRFXXSXXTFIXIXXXMXFF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR002049; Laminin_EGF.
IPR001791; Laminin_G.
IPR000203; PKD_cys_rich.
IPR001368; TNFR_C6.
                                                                                                                                                                    MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, MEGF3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001368; TNE
Pfam; PF00002; 7tm_2; 1.
                                                                                                                                                                                                                                                investigating biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 8; Conserv
                                           SEQUENCE FROM N.A.
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             090YP2
090YP2;
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS0023; CADHERIN.; S. PROSITE; PS00232; CADHERIN.2; 9.
PROSITE; PS00202; EGF_1: UNKNOWN_6.
PROSITE; PS01186; EGF_2: 2.
PROSITE; PS01207; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS02016; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
Calcium-bindding; Call adhasion; EGF-1ike domain; Glycoprotein.
SEQUENCE 2920 AA; 317648 MW; 2919558DF467114F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.3%; Score 35; DB 11; Length 2920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09HCU4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 2923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00008; HormR; 1.
SMART; SM00282; LamiG; 2.
SMART; SW0028; TURR; 1.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro, IPR001881, EGF_Ca.
InterPro, IPR000832, GPCR_secretin.
InterPro, IPR001879; hormn_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR00215; Cadherin.
InterPro; IPR000561; EGF-like.
InterPro; IPR000742; EGF_2.
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InterPro; IPR001203; PKD_cys_rich.
InterPro; IPR001368; TNFR_c6.
Pfam: PF000002; 7tm_2; 1.
Pfam: PF000028; cadherin; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR002049; Laminin_EGF
                                                                             Pfam; PF00008; EGF; 5.
Pfam; PF01025; GPS; 1.
Pfam; PF020793; HRM; 1.
Pfam; PF00054; laminin_G; 2.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                      EGFLAMININ.
GPCRSECRETIN.
     IPR001368; INFR_C6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.58;
                                                                                                                                                                                                                                                                          SMART; SM00112; CA; 9.
SMART; SM00180; EGF_Lam; 1.
SMART; SM00001; EGF_like; 6.
SMART; SM00303; GPS; 1.
                            Pfam; PF00002; 7tm_2; 1.
Pfam; PF00028; cadherin; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:|: || |
|1243 RCVSVLRFDSS 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 54.9
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RCLSIXRFXXS 11
                                                                                                                                                                                                                                                      PRINTS; PR00249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606
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        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Q9HCU4
     NAME OF STREET O
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Usui T., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L.,
Usui T., Shima Y., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L.,
Takeichi M., Uemura T.; transmembrane cadherin, regulates planar cell
polarity under the control of frizzled.";
Cell 98:585-595(1999).
-1- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
-1- SIMILARITY: CONTAINS 9 HARA4070.1;
-1- SIMILARITY: CONTAINS 9 HARA670.1;
-1- SIMILARITY: CONTAINS 9 CAPHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Flamingo 1.
CELSR2 OR FLAMINGO 1.
CELSR2 OR FLAMINGO 1.
Mus musculus (Moouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35; DB 4; Length 2408;
Pred. No. 54;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2408 AA; 261739 MW; EF4BFC2CF993355F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PSO0022; EGF_1; UNKNOWN_6.
PROSITE; PSO1186; EGF_2; 4.
PROSITE; PS50251; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                           SMART; SM00179; EGF_CA; 1.
SMART; SM00001; EGF_Like; 6.
SMART; SM00303; GPS; 1.
SMART; SM00308; HormR; 1.
SMART; SM00282; LamG; 2.
SMART; SM00282; LamG; 2.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 2920 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF_2.
GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hormn_receptor
Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mbsr; roy, ......
1003; MGI:185835; Celsr2.
InterPro; IPR00152; Asx_hydroxyl.
InterPro; IPR002126; Cadherin.
InterPro; IPR000203; PKD_cys_rich.
InterPro; IPR001368; TNFR_c6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001791; Laminin_G.
InterPro; IPR000203; PKD_cys_rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGF-like.
                                             Pfam; PF00002; 7tm_2; 1.
Pfam; PF00002; cadherin; 5.
Pfam; PF00008; EGF; 6.
Pfam; PF00793; HRM; 1.
Pfam; PF00793; HRM; 1.
PRINTS; PR00205; CADHERIN.
PRINTS; PR0010; EGFBLOOD.
                                                                                                                                                                                                                                                                          PRINTS, PRO0011; EGFLAMININ.
SWART; SW00112; CA; 6.
SWART; SW00179; EGF_CA; 1.
SWART; SW0001; EGF_Like; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.3%;
ilarity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              127 RCVSVLRFDSS 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RCLSIXRFXXS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hebeloma cylindrosporum.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Cortinariaceae; Hebeloma.
NCBI_TaxID=76867;
                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                             Strausberger, Strausberger, Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases. RemBL; BC014161; AAH14161.1; "... REMBL; BC01401609; KRAB. InterPro; IPR00082; Znf_C2H2. Refam; PF00096; Zf_C3H2; 11. Recorrer; PS500026; ZINC_FINGER_C2H2_1; UNKNOWN_11. Recorrer; PS50157; ZINC_FINGER_C2H2_2; 11. NAMONAL RECORRER; PS50157; ZINC_FINGER_C3H2_2; 11. NAMONAL RECORRER; PS50157; ZINC_FINGER_C3H2_2; 11. NAMONAL RECORRER 402 AA; 45857 WW; 824FBABAF66609C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.3%; Score 34; DB 4; Length 402; 37.5%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110XFAMS; 115XVO30; MILL; 1.
PROSITE; PS01219; AMMONIUM_TRANSP; UNKNOWN_1.
SEQUENCE 492 AA; 53673 MW; 83E8B1227DFE4064 CRC64;
                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 45.9 kDa protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 3;
Pred. No. 23;
4; Mismatches 13
                                                             402 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        148 RCIECGKFLKKHSTFI 163
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30.4%;
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                                                             PRELIMINARY;
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Best Local Similarity
7; Conserve
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Matches 6; Conserv
                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                     TISSUE-SKIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                          03960
                                                                             096CL0;
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                             RESULT 11
Q96CL0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
Q96UX9
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Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 34; DB 16; Length 106;
Pred. No. 6.3;
1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 2923;
                                                                                                                                                                                                                                                                                                                                                         Calcium-binding; Cell adhesion; Glycoprotein.
SEQUENCE 2923 AA; 317447 MW; 382757D315158ED8 CRC64;
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SEQUENCE 106 AA; 11537 MW; 23BE07040ECBF303 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-WAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                               SM00008; HOTMR; 1.
SM00208; THRR; 1.
SM00208; THRR; 1.
S. PS0010; ASX. HYDROXXL; UNKNOWN_1.
E; PS00232; CADHERIN_1; 6.
E; PS00222; EGF_1; UNKNOWN_6.
E; PS01186; EGF_2; 4.
E; PS01186; EGF_2; 4.
E; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
E; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
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PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 4
Pred. No. 64;
2; Mismatches
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MEDLINE=20512582; Pubmed=11058132;
                                                        PRINTS; PR00205; CADHERIN.
PRINTS; PR00011; BGFLAMININ.
PRINTS; PR000112; CA: 9.
SMART; SM00112; CA: 9.
SMART; SM00101; EGF. 8.
SMART; SM00001; EGF. CA: 5.
SMART; SM00001; EGF. CA: 7.
SMART; SM00001; EGF. Like; 7.
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InterPro; IPR000390; DUF7.
InterPro; IPR001092; HLH_basic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multidrug resistance protein.
            Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRM; 1.
Pfam; PF00054; laminin_G; 1.
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Best Local Similarity 54.5%;
Matches 6; Conservative
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|1242 RCVSVLRFDSS 1252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RCLSIXRFXXS 11
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Best Local Similarity
Matches 8; Conserva
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PROSITE; PS01186
PROSITE; PS50227
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PROSITE;
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                                                                                                                                                                                                                  SMART;
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Q9VWK3;
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                                 Q9CHC5
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Q9VWK3
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RESULT 14
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R.A. Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
R.A. Brandon R.C., Rogars Y.H.C., Blazej R.G., Champe M., Pfelffer B.D.,
R.A. Man M. Basu A. M. Baxendall J., Baytaktaroglu L., Beasley E.M.,
B. Ballew R.W., Basu B.D., Brannan B.P., Bhandari D., Bolshakov S.,
R.A. Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
R.A. Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
R. Borkova D., Botchan M.R., Bulke C., Davenpoolt L., Beasley E.M.,
R. Borkova D., Botchan M.R., Bulke C., Davenpoolt L., Bolshakov S.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenpoolt L.B., Davies P.,
R.A. Cherry J.M., Cawley S., Dahlke C., Davenpoolt L.B., Davies P.,
R. Botton M. B., Gabriellan A.E., Gatry N.S., Gelbart W.M., Classer K.,
R. Godstriellan A.E., Garry N.S., Gelbart W.M., Classer K.,
R.A. Houston K.J., Brandand T.J., Hernandez J.R., Houck J.,
R.A. Kalush F., Karpen G.H., Kee Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Kravitz S., Kulp D., Lai Z.,
Lasko F., Lei Y., Levitsky A.A., Lil Z., Liang Y., Lin X.,
R. Mount S.M. Moy W., Murphy B., Murphy L., Muzry D.M., Nelson D.L.,
R. Melson D.R., Nelson K.A., Nixon K., Worter E., Rang A.H., Rasarding A.C., Siden Kiamos I., Simpson M., Skupski M.P., Sanith T.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Sanith T.,
R. Shier E., Spradling A.C., Stapleton M., Zhong G., Zhao Q., A.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q., A.,
R. Hilliams S.M., Woodage T., Worley C., Wu D., Yang S., Zhao C.,
R. Firent K. Teckor C., Turner R., Vanter J.C.;
R. Heiner K. Benington M., Shupski M.P., Shith H.O.,
R. Heiner K. Benington M., Shupski M.P., Shith H.O.,
R. Hilliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao C., Shen Kianser B.C., Shen Ki
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                                                                                                                                                                                                          Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Pfam; PF01757; Acyl_transf_3; 1.
SEQUENCE 700 AA; 78477 MW; 3514BF1A51A43610 CRC64;
                                                                                                01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
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                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                    STRAIN=BERKELEY;
MEDLINE=20196006; Pubmed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FlyBase; FBgn0031034; CG14205
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                                                                  PRELIMINARY;
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Best Local Similarity
7; Conserv?
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                    CG14205 protein.
                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
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                                                                                 09VWG4;
                                                                 Q9VWG4
                               RESULT 13
                                                  09VWG4
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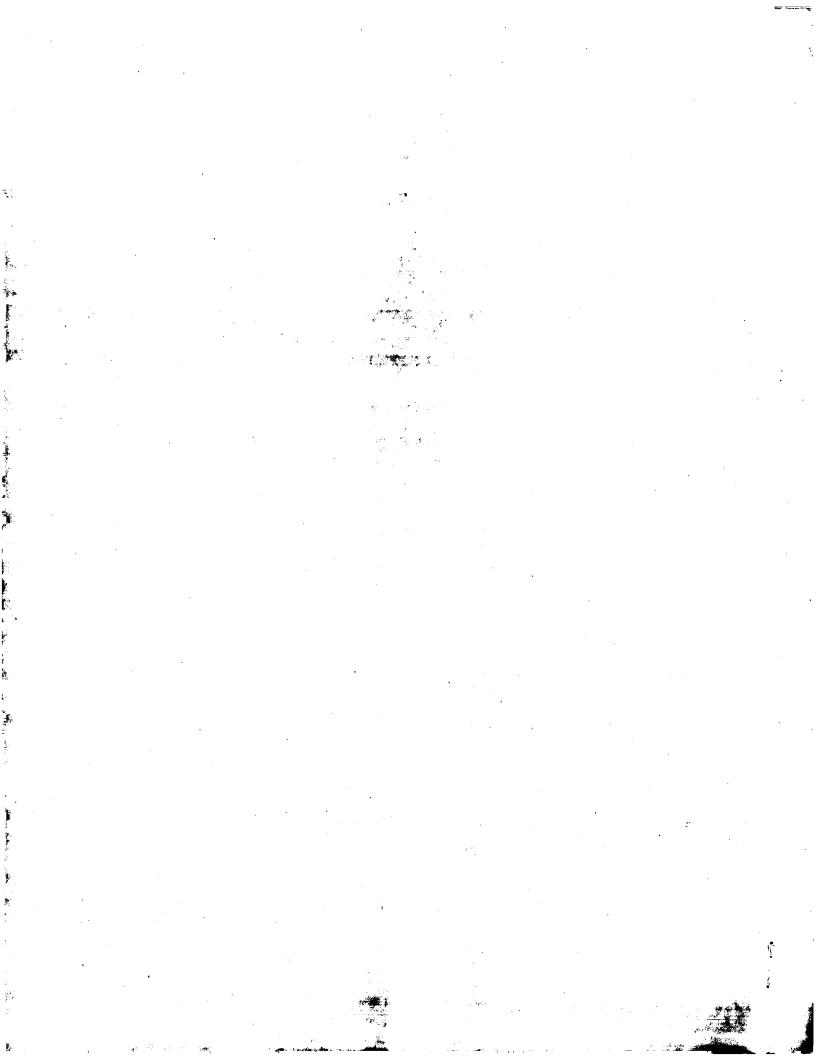
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REDIENCE TROUGH N. S. COLORNE FROM N. S. COLORNE FROM N. S. COLORNE FROM N. S. COLORNE FROM N. S. C. SCHERE S. E., HOIL R. A., Evans C. A., Gocayne J. D., A dams M. D. Celniker S. E., HOIL R. A., Hoskins R. A., Galle R. F., Ceorge R. A., Levis S. E., Richards S. Ashburner M., Henderson S. N., Sutton G. G., Wortman J. R., Yandell M. D., Zhang Q., Chen L. X., A sutton G. G., Wortman J. R., Yandell M. D., Calmpe M., Pfelifer B. D., An K. H., Doyle C., Baxter E. G., Helt G., Nelson C. R., Miklos G. L. G., Abril J. F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D., A abril J. F., Bason R. Y., Berman B. P., Bhandari D., Bolshakov S., Ballew R. M., Basu A., Burker J. B., Bortstein P., Bortstein P., Bortswa D. N., Butch T., Cadieu E., Center A., Chandra I., A Burtis K.C., Busam D. A., Butler H., Cadieu E., Center A., Chandra I., A Borson K., Dowl L. E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn P., Dorson K., Doup L. E., Downes M., Dugan-Rocha S., Dunkov B. C., Dunn P., Dorson K., Doup L. E., Downes M., Dugan-Rocha S., Pleischmann M., Rodek A., Gong F., Garrell J. H., Gu Z., Guan P., Harris M., Harris M., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                     MEDLINE-21235186; PubMed=11337471;
MEDLINE-21235186; PubMed=11337471;
MEDLINE-21235186; PubMed=11337471;
MEDLINE-21235186; PubMed=11337471;
Medsenbach A., Ehrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis 11.4403.";
Genome Res. 11.731-75(2001).
EMBL; AE006314; AAK04905.1;
InterPro; IPR001117; Cu-oxidase.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                       Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%; Score 33; DB 16; Length 393;
26.1%; Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 AA; 43617 MW; 3BD755460656204C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 AA.
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| 154 ISFERFRASIFLFLSLVLNLLYF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
                                                    Created)
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                                                                                                                                                                                                                                 Streptococcaceae; Lactococcus.
                                                                         01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                           Unknown protein.
YIBE OR LL0807.
                                                                                                                                                                                                                                                      NCBI_TaxID=1360;
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                                               01-JUN-2001
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RA Hostin D., Houston K.A., Howland T.J.; Wei M.-H., Ibegwam C.,
RA Jalain M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Klulp D., Lai Z.,
RA Liu X., Matteri B., McnThosh T.C., Mcneod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarty C., Mcnriso J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Alazzolo M., Pittuma G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Shier B., Spradling A.C., Stapledor M., Stupski M.P., Smith T.,
Shier E., Spradling A.C., Stapledor M., Stupski M.P., Smith T.,
Shier B., Spradling A.C., Stapledor M., Stupski M.P., Smith T.,
RA Shier B., Spradling A.C., Stapledor M., Stupski M.P., Smith T.,
Shier B., Spradling A.C., Stapledor M., Stupski M.P., Smith T.,
Shier B., Spradling A.C., Stapledor M., Stupski M.P., Smith T.,
RA Shier B., Spradling A.C., Stapledor M., Stupski M.P., Smith T.,
Shier B., Spradling A.C., Stapledor M., Stupski M.P., Smith H.O.,
RA Wang Z.-T., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-T., Wassarman D.A., Worler E., Wang A.H., Wang X.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zhao Q., Zhao G. A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhao L.,
Science 287:218-2195(2000)
DR REMBL; AEGO351; Ang W., Wonter J.C.;
REMBL; AEGO351; Ang W., Wonter J.C.;
REMBL; AEGO351; Ang W., Wonter J.C.;
REMBL; AEGO351; Ang W., Zhong W., Zhu S., Zhu X., Smith H.O.,
DR REMBL; AEGO351; Chitin_bind_PerA.
DR SWART; SMO494; Chitin_bind_PerA.
DR SWART; SMO494; Chithin_bind_PerA.
Best Local Similarity 42.9%; Pred: No. 38; Length 481;
Best Local Similarity 42.9%; Pred: No. 38; Indels 0; Gaps 0;
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Search completed: July 16, 2003, 17:49:59 Job time: 10.7707 secs

2 CLSIXREXXSXXTF 15 |||:|| || 342 CLSVGRFAGIDETY 355

상 음



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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:36:24 ; Search time 8.95784 Seconds Run on:

(without alignments)
476.010 Million cell updates/sec

US-09-853-079-39 108 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

A_Geneseq_101002:*

| SIDS2/gcddata/geneseq/geneseqp-embl/AA1980.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1986.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1986.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1980.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1980.DAT:*
| SIDS2/gcddata/geneseqy-geneseqp-embl/AA1980.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-geneseqp-embl/AA1981.DAT:*
| SIDS2/gcddata/geneseqy-geneseqp-embl/AA1982.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1982.DAT:*
| SIDS2/gcddata/geneseqy-embl/AA1982.DAT:*

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1993.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1994.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1995.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1996.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1997.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1998.DAT:*/SIDS2/gcgdata/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/SIDS2/geneseqp-embl/AA1999.DAT:*/S /SIDS2/gcgdata/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /gcgdata/geneseq/geneseqp-emb1/AA2001 18:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA2002.DAT:*

SUMMARIES

					CHTANAMOO	
		æ				
Result		Query				
NO.	Score	_	Match Length DB	DB	ID	Description
-	82	75.9	:	19	AAW56298	Babesia microti BM
7	82	75.9		20	AAY24358	Babesia microti an
٣	82	75.9	445	7	AAB30207	B. microti BMNI-17
4	82	75.9		23	ABB88952	Babesia microti an
ស	82	75.9		23	ABB89025	Babesia microti an
9	82	75.9		21	AAB30230	B. microti MN-10/B
7	82	75.9		23	ABB88975	Babesia microfi an
8	82	75.9		23	ABB88989	Babesia microti an
6	82	75.9	Н	21	AAB30231	B. microti MN-10/B
10	82	75.9	_	23	ABB88976	Babesia microti an

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AAY24359 ABB30208 ABB30208 ABB30208 AAY24365 ABB30217 ABB30213 ABB89013 ABB89013 ABB89013 ABB89010	AAB94420 AAB94420 AAY31988 AAU00225
222222222222222222222222222222222222222	2022
322 322 2752 2752 2752 2752 2752 2752 27	914 407 407
44446664666666666666666666666666666666	32.4 32.4 32.4
88 88 88 88 88 88 88 88 88 88 88 88 88	988
11111111111111111111111111111111111111	1 4 4 4 2 4 4 5

ALIGNMENTS

AAW56298 standard; Protein; 445 AA AAW56298; RESULT 1 AAW56298

28-SEP-1998 (first entry)

Babesia microti BMNI-17 complement antigen sequence.

antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.

Babesia microti.

EP834567-A2.

97EP-0117067. 01-OCT-1997; 08-APR-1998.

97US-0845258. 96US-0723142. 24-APR-1997; 01-OCT-1996;

(CORI-) CORIXA CORP

Sleath PR; Reed SG, Houghton R, Lodes MJ,

WPI; 1998-195465/18. N-PSDB; AAV22753.

Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid,

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75.9%;
56.2%;
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56.2%;
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17-MAR-2000; 2000US-0528784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2000; 2000WO-US09136.
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                                                                                          Conservative
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                         Query Match
Best Local Similarity
Thes 18; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babesiosis; rodent
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nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                     AAB30207;
      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia microti antigen BMNI-17 complementary open reading frame protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAV24327 to AAY2438 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence encodes a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
    transformed cells and antibodies, useful for diagnosis of
                                                                                                 The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 82; DB 19;
Pred. No. 5.5e-09;
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                         infection and in protective vaccines
                                                               Claim 1; Page 77-79; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY24358 standard; Protein; 445 AA.
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56.2%;
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Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunity; detection
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                                                                                                                                                                                                                                                                                                                                                                                                  445 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective
                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. microti BMNI-17 antigen reverse complement SEQ ID NO: 38.
Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McNeil1
Score 82; DB 20;
Pred. No. 5.5e-09;
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                                                                                                                                   244 GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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Pred. No. 5.5e-
0; Mismatches
                                                    Mismatches
                                                                                                     1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 86-87; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton RL,
                                                                                                                                                                                                                                                                                        AAB30207 standard; Protein; 445
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Homer MJ;

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The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                 New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections \,
                                                                                                                          McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 23;
6e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sleath PR,
                                                                                                                          Sleath PR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 82; DB 2
Pred. No. 6e-09
0; Mismatches
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                                                                                                                                                                                                                                                                                          Claim 2; Page 191-192; 195pp; English.
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                                                                                                                          Lodes MJ, Houghton RL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999
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Best Local Similarity 56.2%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB30230 standard; Protein;
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17-MAR-2000; 2000US-0528784
               10-OCT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0737178.
26-FEB-2001; 2001US-0794764.
07-SEP-2000; 2000US-0656688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-686939/67
                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                               WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 AA;
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Synthetic.
                                                                                                                                             Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                             SG,
                                                                                                                             Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                         Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   infection. The present sequence was used to illustrate the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                       Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                       McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.9%; Score 82; DB 23; Length 445; 56.2%; Pred. No. 5.5e-09; Live 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti antigenic epitope fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                       Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB89025 standard; Protein; 481 AA
                   Babesia microti antigen epitope #1
                                                                                                                                                                                                                                                                                                                                                                                                       Lodes MJ, Houghton RL,
                                                                                                                                                                                                                                   2000US-0569098.
2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0794764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.9
Best Local Similarity 56.2
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-216691/27.
                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         445 AA;
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                                                                                         Babesia microti
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07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
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Secrist H;
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ABB8902 RESULT

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Best Local Similarity
Matches 18; Conserv
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Secrist H;
           465
                                                                                                            ABB88989;
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                                                    RESULT 8
ABB88989
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        The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
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                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homer
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0
                                                                                                                                                                                                                                                                                                                                                                                                             vaccine; antigen; antigenic epitope; infection.
                                                                                                                                        Length 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 666;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                               Babesia microti antigenic epitope fusion protein BaF-3.
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                                                                                                                                     Score 82; DB 21; L
Pred. No. 8.8e-09;
0; Mismatches 14;
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                                                                                                                                                                                                                GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 496
                                                                                                                                                                                            1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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Pred. No. 8.8e-0; Mismatches
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                                                                                                                                                                                                                                                                                             ABB88975 standard; Protein; 666
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2000US-0605724.
2000US-065688.
2000US-0685436.
2000US-0731778.
                                                                                                                                     75.9%;
56.2%;
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56.2%;
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                                                                                                                                                                 Conservative
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                                                                                                                                     Query Match
Best Local Similarity
Matches 18; Conserv
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hes 18; Conserv
                                                                                                           666 AA;
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13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                         ABB88975;
                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                 RESULT 7
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Homer MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing
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                                                                                                                                                                                                             Protozoacide; vaccine; antigen; antigenic epitope; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babesiosis; rodent parasite; tick-borne illness; antigen;
                                                                                                                                                         Babesia microti antigenic epitope fusion protein BaF-5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.9e-09;
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Pred. No. 8.9e-09;
0; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microti infection, and as component of a compound immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 35; Page 160-163; 195pp; English
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ABB88989 standard; Protein; 677
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56.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27-JUN-2000; 2000US-0605724.
07-SEP-2000; 2000US-0656688.
10-OCT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0737178.
26-FEB-2001; 2001US-0794764.
                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-2001; 2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0569098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-216691/27.
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such
                                                                                                                                                                                                                    The present invention relates to novel Babesia microti antigens and to coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                     Homer MJ;
                                                                                                         New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                           Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babesia microti antigen BMNI-17 degenerate repeat sequence.
                     McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                               14;
                                                                                                                                                                                                                                                                                                                                                                                         75.9%; Score 82; DB 23; 56.2%; Pred. No. 1.6e-08;
                   Sleath PR,
                                                                                                                              microti infection, and as component of a compinmune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                    Page 116-120; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
3
                     Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ā
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Misc-difference 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'label= Gly, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= Lys, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abel= Glu, Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= Ile, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            label= Thr, Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Ilr, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY24359 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'label= Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 label= Pro,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Cys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                       Query Match 75.9
Best Local Similarity 56.2
Matches 18; Conservative
                      Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunity; detection.
                                                                        WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                                                                                       1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Misc-difference 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1999
                                        Secrist H;
                                                                                                                                                                                      Claim 35;
                                                                                                                                                                                                                                                                                                                                                       Sequence
                     SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY24359;
                     Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY24359
     Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                  New polypeptides containing an antigenic portion of Babesia microti
antigen and DNAs encoding the polypeptides, useful for diagnosing,
treating or preventing B. microti infection, or for inducing protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1132;
                                                                                                                                                                                                                                                                                                 McNeill PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesia microti antigenic epitope fusion protein BaF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 82; DB 21;
Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                             Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 7; Page 112-116; 118pp; English.
disease diagnosis; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABB88976 standard; Protein; 1132 AA
                                                                                                                                                                                                                                                                                             Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.9%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0569098.
2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0731718.
                                                                                                                                                                                                 05-APR-1999; 99US-028648B
17-MAR-2000; 2000US-0528784.
                                                                                                                                                               05-APR-2000; 2000WO-US09136
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                                                                                                                                                                                                                                                                                                                                                                                                                             a patient
                                                                                                                                                                                                                                                                                                                                WPI; 2000-686939/67.
                                                                                                                                                                                                                                                                                             Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia microti.
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                                                                                      WO200060090-A1
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                                                                                                                          12-OCT-2000
                                    Babesia sp
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                             Reed SG,
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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malariar like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis,
antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient \,
                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protozoacide; vaccine; antigen; antigenic epitope; infection
                                                                                                                                                                                                                                                                                                                                                           Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                      ore 80; DB 21;
red. No. 7.1e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                              prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babesia microti antigen epitope repeat.
                                                                                                                                                                                                                                                                                                                                                           Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                               Claim 6; Page 88; 118pp; English.
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m Thr}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Lys,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label- Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label= Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'label- Glu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label- Pro,
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 32; Conser
                                                                                                                                                                                                                                                                                                            32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
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                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY2433 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B. microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides containing an antigenic portion of Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ID NO: 39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 32;
                                                                                                                                                                                                                                                                                                            SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B. microti BMNI-17 antigen reverse complement repeat SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McNeil1
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                                                                                                                                                                                                                                                                                                            Persing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 80; DB;
Pred. No. 7.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 94; 126pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.1%; Scur.
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB30208 standard; Peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghton RL,
/label= Cys, His
                                                                                                                                           98WO-US26437
                                                                                                                                                                                       97US-0990571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                            Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Conservative
                                                                                                                                                                                                                                                              (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-385612/32.
                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babesiosis; rodent
disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200060090-A1.
                                              W09929869-A1
                                                                                                                                           11-DEC-1998;
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                                                                                                                                                                                                                                                                                                            Bruinsma E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2001
                                                                                            17-JUN-1999
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                                                                                                                                                                                                                                                                                                                                  Sleath PR;
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AAB30208
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infection and in protective vaccines
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                                                                                                                                                                                             Best Local Similarity 56.2
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-385612/32.
N-PSDB; AAX90017.
                                                                                                                                                                                                                                                                                                                                                                                immunity; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORI-) CORIXA CORP
                                                                                                                                                                275 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                    Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                     WO9929869-A1
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                                                                                                                                                                                                                                                                                                               AAY24365;
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                                                                                                                                                                  Sequence
                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                          RESULT 15
                                                                                                                                                                                                                                                                                   AAY24365
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                                                                                                                                                                                                     The present invention relates to novel Babesia microti antigens and their
                                                                                                                                                                                                              coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                Homer MJ;
                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                           New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                              ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                              McNeill PD,
                                                                                                                                                                                                                                                                                            Length 32;
                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                 Score 80; DB 23; Le
; Pred. No. 7.1e-10;
                                                                                              Sleath PR,
                                                                                                                                                                                                                                                                                                                                          1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti BMNI-20 antigen sequence.
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                                                                                              Houghton RL,
                                                                                                                                                                                                                                                                                   74.1%; Sco.
100.0%; Pre
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                                                                                                                                                                                   Claim 7; Page 94; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  AAW56303 standard; Protein; 275
        10-MAY-2000; 2000US-0569098.
27-JUN-2000; 2000US-065524.
07-SEP-2000; 2000US-0656688.
10-OCT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0731778.
26-FEB-2001; 2001US-0794764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97EP-0117067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0845258.
96US-0723142.
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                              Lodes MJ,
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                                                                          (CORI-) CORIXA CORP
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                                                                                                                          WPI; 2002-216691/27
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                        32 AA;
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                           07-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-APR-1998
                                                                                                         Secrist H;
                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     AAW56303;
                                                                                              Reed SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   specific immunogenic portions of Babesia microti. AAX88981 to AAX889994 encode specifically claimed B. microti immunogenic proteins, and AAY44317 to AAY4338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                                                                one addition to portion of a Babbasia microti antigen. Trean be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       present invention describes isolated polypeptides comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 275;
                                                                        sequence is that of a polypeptide comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 79; DB 19;
Pred. No. 1.4e-08;
0; Mismatches 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Persing D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 109-110; 126pp; English.
Claim 1; Page 101-102; 113pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY24365 standard; Protein; 275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.18;
56.28;
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us-09-853-079-39.rag

0; Gaps Query Match 73.1%; Score 79; DB 20; Length 275; Best Local Similarity 56.2%; Pred. No. 1.4e-08; Matches 18; Conservative 0; Mismatches 14; Indels

. 0

216 GHGKPNTNKSEKAERKSHDTQTTQEICEECEE .247 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32

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Search completed: July 16, 2003, 17:46:44 Job time: 9.95784 secs

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July 16, 2003, 17:42:54; Search time 2.914 Seconds (without alignments) 323.107 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                      OM protein - protein search, using sw model
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US-09-853-079-39 108 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32 Title: Perfect score: Sequence:

262574 seqs, 29422922 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

262574 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

/cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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,	Appl	App1	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appl	Appli	Appli	Appli	3746, Ap	Appli	Appl	Appli	Appli	5080, Ap	Appl	Appl	Appli	Appli	Appl
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ES	-258-38	-723-142A-38	784A	784A	784A	258-	1434	784A	258-	571-	784A	172-	361-	274-	001C	438A	438A	952-	300-	001C	340-	329-	271-	271-	811-
SUMMARIES	845	-723-	-528-	-528-	-528-	-845	7 2 2 2	-528-	-845-	-066-	-528-	-800-	-210-	-740-	-134-	-271-	-271-	-326-	-363-	-134-	-897-	-252-	-482-	-482-	-854-
SQI TD	US-08-845-258-38	02-08 03-08	US-09-528-784A-38	US-09-528-784A-8	US-09-528-784A-87	US-U8-845-258-39	US-U8-330-3/1-39	US 08 /23 1428-39	US-08-845-258-53	US-08-990-571-53	US-09-528-784A-5	US-09-008-172-	US-09-210-361-6	US-09-740-274-6	US-09-134-001C-3746	US-09-271-438A-4	US-09-271-438A-1	US-09-356-952-5	US-08-363-300-2	US-09-134-001C-5080	US-08-897-340-3	US-09-252-329-3	US-08-482-271	US-08-482-27	0S-08
DB	4 <	. 4	4	4	→ .	4 •	* ~	* 4	4	4	4	٣	4	4	4	4	4	m	H	4	7	4	Н	Н	7
Length DB	445	445	445	999	1132	25.0	200	3.5		275	275	1430	1430	1430	262	407	407	1048	1141	3696	245	245	264	264	264
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Length 445; 14; Indels

Score 82; DB 4; I Pred. No. 1.3e-09; 0; Mismatches 14;

75.9%; s milarity 56.2%; F Conservative 0;

Query Match Best Local Similarity Matches 18; Conserva

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Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 27, Appli Sequence 7, Appli Sequence 7, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 2, Appli Sequence 2, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli	INFECTION INFECTION	
US-09-080-120A-2 US-09-080-120A-4 US-09-322-484-1 PCT-US95-089-25-1 PCT-US95-08925-2 PCT-US95-08925-4 US-09-177-165A-27 US-09-080-120A-7 US-09-177-165A-27 US-09-177-165A-24 US-09-177-179-5 US-09-177-179-5	ALIGNMENTS 5258 SAND METHODS FOR THE TWENT OF B. MICROTI er, 701 Fifth Avenue 8-DOS #1.0, Version #1.30 845,258	
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264 264 264 264 264 272 272 272 272 272 273 273 273 273 273	llication US/0884; 76 eed, Steven G. eed, Michael J. oddes, Michael J. oughton, Raymond leath, Paul R. WIION: COMPOUND WITON: AND TREAY UENDES: 53 EED AND BERRY 00 Columbia Cent. tile hington SA ABLE FORM: : Floppy disk IIBM PC compatibl ISM PC COMPOUND ISM INFORMATION: . 24-APR-1997 ION: 435 ION:	
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311111111111111111111111111111111111111	1 10.5-258-38 to 10.61839 th 10.61839 th 10.61839 th 10.61839 th 10.61839 PPLICANT: Replicant: Splicant: Spli	0
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APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROII INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 445;
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APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 82; DB 4;
Pred. No. 1.3e-09;
0; Mismatches 14
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Pred. No. 1.3e-09;
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CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
SUUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                           REFERENCE/DOCKET NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
TELEFAX: (206) 682-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 38:
                              UMBER: US/08/723,142A
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 38, Application US/09528784A Patent No. 6451315 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 85, Application US/09528784A Patent No. 6451315 GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Lodes, Michael J.
                                  APPLICATION NUMBER: US/08/723
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEX/AGENT INFORMATION:
NAME: MAKL, DAVID J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
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56.2%;
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56.2%;
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LENGTH: 445 amino acids
TYPE: amino acid
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Best Local Similarity 56.29
Matches 18; Conservative
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Best Local Similarity 56.2
Matches 18; Conservative
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US-08-723-142A-38
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                                                                Sequence 38, Application US/08990571

Patent No. 6214971

GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
UNMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
STREET: 6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 1.3e-09;
0; Mismatches 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 38, Application US/08723142A
Patent No. 6306396
GERERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND ME
TITLE OF INVENTION: AND TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WIMBER: US/08/990,571
11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CAMPUTTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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56.2%;
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(206)682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 56.29
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 CC.
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                      STATE: Washington COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1. CLASSIFICATION:
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US-08-723-142A-38
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US-08-990-571-38
                                                      US-08-990-571-38
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NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /note= "Residue can be either Pro
OTHER INFORMATION: or Ile"
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or Thr"
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or Arg"
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or Thr"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGFWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATE:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: MAKI, DAVId J.
REGISTRATION NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (2006) 622-4900
TELEPHONE: (2006) 622-4900
TELEFRONE: (2006) 622-4900
TELEFRONE: (2006) 622-4900
TELEFRONE: (2006) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acid
STRANBEDNESS:
TOPOLOGY: linear
FEATURE:
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LOCATION: 7
OTHER INFORMATION: /note-
OTHER INFORMATION: or Thr'
FEATURE:
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NAME/KEX:
NAME/KEX:
LOCATION: 14
LOCATION: And OTHER INFORMATION: Or GIY
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LOCATION: 12
OTHER INFORMATION: /note
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LOCATION: 23
OTHER INFORMATION: /note
OTHER INFORMATION: or Pr
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27
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LOCATION: 3
OTHER INFORMATION: /note
OTHER INFORMATION: or As
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION:
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: McMeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 21012.1.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 39, Application US/08845258
Patent No. 6183976
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE SEED AND BERRY
ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 75.9%; Score 82; DB 4; Length 1132; Best Local Similarity 56.2%; Pred. No. 3.8e-09; Matches 18; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                               Length 666;
                                                                                                                                                                                                                                                                                          14; Indels
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                                                                                                                                                                                                                                             Query Match 75.9%; Score 82; DB 4;
Best Local Similarity 56.2%; Pred. No. 2.1e-09;
Matches 18; Conservative 0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                        1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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    FILE REFERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 87, Application US/09528784A Patent No. 6451315 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seattle
Washington
                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Babesia
US-09-528-784A-85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Babesia
US-09-528-784A-87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-528-784A-87
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OTHER INFORMATION: /note= "Residue can be either Pro OTHER INFORMATION: or Ile"
                                                                                                                                                              LOCATION: 11
OTHER INFORMATION: /note= "Residue can be either Glu
OTHER INFORMATION: or Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Residue can be either Ile
or Thr"
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                                                                                         /note= "Residue can be either Lys or Thr"
                                                                                                                                                                                                                                                                          /note= "Residue can be either Lys
                                                                                                                                                                                                                                                                                                                                                                    /note= "Residue can be either Glu or \operatorname{Gl} y
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Residue can be either Ile
or Arg"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Residue can be either Thr or Pro"
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or Glu"
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illarity 100.0%; Pred. No. 1.9e-1
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                             or Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: 23
OTHER INFORMATION: /note-
OTHER INFORMATION: or Pro'
FEATURE:
NAME/KEY: Modified-site
LOCATION: 26
OTHER INFORMATION: /note-
OTHER INFORMATION: or Thr'
FEATURE:
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OTHER INFORMATION: /note-
OTHER INFORMATION: or Ser'
FEATURE:
NAME/KEY: Modified-site
LOCATION: 28
                                  FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
                                                                                                                                                                                                                                      Modified-site
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NAME/KEY: Modified-site
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                      NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                  FATURE:
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Patent No. 6214971
GENERAL INFORMATION
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia.Center, 701 Fifth Avenue
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/note= "Residue can be either Cys or Ser"
                                                                                 /note= "Residue can be either Asp
or Glu"
                                                                                                                                                                                 /note= "Residue can be either Glu
or Ala"
                                                                                                                                                                                                                                                                  /note= "Residue can be either Cys
or His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Residue can be either Gly or Asp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECPHONE: (206) 622-4900
TELEPRAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UMBER: US/08/990,571
11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (206) 622-4900
TELEFRAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acids
STRANDEDNESS:
                                             NAME/KEY: Modified-site
LOCATION: 28
LOCATION: 28
COTHER INFORMATION: Or Glu'
FEATURE:
NAME/KEY: Modified-site
LOCATION: 29
COTHER INFORMATION: /note=
                                                                                                                                                                                                                                    NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: Modified-site LOCATION: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDALL
STREET: 6300
CITY: Seattle
STATE: Washington
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                  OTHER INFORMATION:
COTHER INFORMATION:
US-08-845-258-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-990-571-39
                                                                                                                                                                                                                                                         LOCATION:
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NAME/KEY: Modified-site
LOCATION: 5
OCHER INFORMATION: /note="Residue can be either Pro
OTHER INFORMATION: or 11e"
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                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compartible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                           E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MAK!, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426
TELECOMUNICATION INFORMATION:
TELECHONE: (206) 622-4900
TELECHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-4901
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acids
STRANDEDNESS:
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                                                                                                                                                                                        NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND B
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OTHER INFORMATION:
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Washington
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                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 98104
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LOCATION:
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STATE:
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Moweill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42664
CURRENT APPLICATION NUMBER: US/09/528,784A
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/note= "Residue can be either Ile
or Arg"
                                                                                           /note= "Residue can be either His or Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Residue can be either Asp
or Glu"
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or Pro"
                                                                                                                                                                                                                                                                                                                                                                                   /note= "Residue can be either Cys or Ser"
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or His"
                                                                                                                                                                                                                                                                             /note= "Residue can be either or Thr"
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 39
LENGTH: 32
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Patent No. 6451315
                                   FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: Or Tyr'
FEATURE:
NAME/KEY: Modified-site
LOCATION: 23
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) LOCATION: 30
OTHER INFORMATION: /note
) OTHER INFORMATION: or Hi
US-08-723-142A-39
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LOCATION: 26
OTHER INFORMATION: /note
OTHER INFORMATION: or Th
                                                                                                                                                                                                                                                                                                                                    Modified-site
27
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NAME/KEY: Modified-site
LOCATION: 28
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FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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LOCATION: (3)...(3)
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LOCATION:
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GENERAL INFORMATION:
APPLICANT: Read, Steven G. et al.
TITLE OF INTENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. NUMBER OF SEQUENCES: 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79; DB 4; Pred. No. 3.4e-09;
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                                                                                  FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David.J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 53, Application US/08990571 Patent No. 6214971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear _
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Babesia Microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.18;
56.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Babesia Microti
                                                                                                                                                                                                                                                                                                                                       275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (206)682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-845-258-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                   LENGTH:
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APPLICANT: Reed, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SPED AND BERRY
ADDRESSEE: SPED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.1%; Score 80; DB 4; Length 32; 100.0%; Pred. No. 1.9e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ION: (28)...(28)
INFORMATION: Xaa = Aspartic Acid or Glutamic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
INFORMATION: Xaa = Glycine or Aspartic Acid
                                                                                                                                                                         ION: (11)...(11)
INFORMATION: Xaa = Glutamic Acid or Glycine
                                                                                                                                                                                                                                                                                                            ION: (14)...(14)
INFORMATION: Xaa = Glutamic Acid or Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (29)...(29)
OTHER INFORMATION: xaa - Glutamic Acid or Alanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Isoleucine or Threonine
                                                                                                                                                                                                                                                                                                                                                                          ON: (15)...(15)
INFORMATION: Xaa = Isoleucine or Arginine
                                      LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = Proline or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; LOCATION: (30)...(30)
; OTHER INFORMATION: Xaa = Cysteine or Histidine
US-09-528-784A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = Histidine or Tyrosine
                                                                                                                                                                                                                       LUCATION: (12)...(12)
OTHER INFORMATION: Xaa = Lysine or Asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ION: (23)...(23)
INFORMATION: Xaa = Threonine or Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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                                                                                                         LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = Lysine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
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THER INFORMATION: Xaa = Cysteine or Serine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 74.1 Best Local Similarity 100. Matches 32; Conservative
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MEDIUM TYPE: Floppy
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CITY: Seattle
STATE: Washingt
                                                                                                                                                       NAME/KEY: VARIANT
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Search completed: July 16, 2003, 17:51:00 Job time: 3.914 secs
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                                                                                                                                                                                                                                              Sequence 53, Application US/09528784A

Patent No. 6451315

GENERAL INPORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Aleath, Paul R.
APPLICANT: Moughton, Raymond L.
APPLICANT: Moughton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Moughton, Raymond L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42664
CURRENT APPLICATION NUMBER: US/09/528,784A

CURRENT APPLICATION NUMBER: US/09.528,784A

NUMBER OF SEQ ID NOS: 90

NUMBER OF SEQ ID NOS: 90

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 1430;
                                         Length 275;
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TITLE OF INVENTION: Substitutes for Modified Starch and
TITLE OF INVENTION: Latexes in Paper Manufacture
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0388D
CURRENT PAPLICATION NUMBER: US/09/008,172
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTEED for Windows Version 3.0
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                                       Score 79; DB 4; I
Pred. No. 3.4e-09;
0; Mismatches 14;
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Pred. No. 3.4e-09;
0; Mismatches 14
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4; Mismatches
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Patent No. 6127602
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: Streptococcus mutans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.18;
56.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36.1%; 27.6%;
                                       73.1%;
56.2%;
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Best Local Similarity 56.23
Matches 18; Conservative
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                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
CORGANISM: Babesia microti
US-09-528-784A-53
                                     Query Match
Best Local Similarity
Matches 18; Conserva
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Matches 8; Conserv
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US-09-528-784A-53
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US-08-990-571-53
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LENGTH: 275
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                                                       GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0357CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17;
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Pred. No. 6.5;
4; Mismatches
                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/210,361
CURRENT PELLING DATE: 1998-12-11
CURRENT PILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER PILING DATE: 1998-009,620
EARLIER PILING DATE: 1998-01-20
EARLIER PILING DATE: 1998-01-20
EARLIER PELLING DATE: 1998-01-20
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER PELLING DATE: 1998-01-20
EARLIER PELLING DATE: 1998-01-16
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Sequence 6, Application US/09210361
Patent No. 6284479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: streptococcus mutans US-09-210-361-6
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Best Local Similarity 27.6
Matches 8; Conservative
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Sequence 38, Appl
Sequence 38, Appl
Sequence 211, App
Sequence 85, Appl
Sequence 144, App
Sequence 144, App
Sequence 147, Appl
Sequence 37, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 53, Appl
Sequence 195, Appl
                                                                                                                                                           July 16, 2003, 17:47:39; Search time 5.2344 Seconds (without alignments) 726.026 Million cell updates/sec
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/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/ cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US00_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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US-09-853-079-202
US-09-853-079-195
US-09-853-079-194
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US-09-853-079-87
US-09-737-178-87
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US-09-286-488-53
US-09-853-079-53
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US-09-853-079-144
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US-09-853-079-85
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US-09-853-079-38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published_Applications_AA:*
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Maximum Match 100%
Listing first 45 summaries
                                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match Length
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Gaps

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Length 445; Indels

Score 82; DB 9; Pred. No. 6.7e-09;

75.9%; 56.2%;

Query Match 75.9° Best Local Similarity 56.2° Matches 18; Conservative

; ORGANISM: Babesia microti US-09-286-488-38

TYPE: PRT

0; Mismatches

1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32

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Sequence 38, Application US/09853079. Publication No. US20030109689A1 GENERAL INFORMATION:

RESULT 2 US-09-853-079-38

APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.

Sequence 199, App Sequence 198, App Sequence 193, App Sequence 203, App1 Sequence 203, App1 Sequence 2, App11 Sequence 10, App1 Sequence 11455, App Sequence 11617, A Sequence 1156, App Sequence 12664, A Sequence 12664, A Sequence 12664, A Sequence 12664, A Sequence 1366, A Sequence 1366, A Sequence 3, App11 Sequence 3, App11 Sequence 3, App11 Sequence 3, App11 Sequence 38, Application US/09286488

Patent No. US20020169136A1

Sequence 1 NFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: Beath, Paul R.

APPLICANT: McNeill, Patricia D.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 210.12.1.4.26C3

CURRENT APPLICATION NUMBER: US/09/286,488

CURRENT APPLICATION NUMBER: US/08.286,488

WUMBER OF SEO ID NOS: 83

NUMBER OF SEO ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 3.0 US-09-853-079-199 US-09-853-079-198 US-09-853-079-198 US-09-853-079-193 US-09-853-079-193 US-09-853-079-193 US-09-853-079-197 US-10-74-409-2 US-10-077-751-2 US-10-077-751-2 US-10-115-023-4 US-10-115-023-4 US-10-115-023-4 US-09-184-208-4 US-09-184-208-4 US-09-181-9864-5330 US-09-181-9864-5330 US-09-815-242-116455 US-09-815-242-116455 US-09-815-242-116455 US-09-815-242-116455 US-09-815-242-5914 US-09-815-242-12664 US-09-815-242-13160 US-09-925-301-1156 US-09-956-508A-3 US-09-956-508A-3 ALIGNMENTS 10 22 4407 4407 4407 5597 5597 805 91 91 91 US-09-286-488-38 SEQ ID NO 38 LENGTH: 445

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                                                                                                                                                                                                           Score 82; DB 9; 1
Pred. No. 7.2e-09;
0; Mismatches 14
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI
FILE REFERENCE: 210121 426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 201-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
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Pred. No. 1e-08;
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    CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FASELSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEG ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 3.0
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, Sequence 85, Application US/09853079

; Publication No. US20030109689A1

; GENERAL INFORMATION:
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Houghton, Raymond L.
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Lodes, Michael J.
Houghton, Raymond L.
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McNeill, Patricia D.
Homer, Mary
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McNeill, Patricia D.
Homer, Mary
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56.2%;
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Best Local Similarity 56.2%;
Matches 18; Conservative
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Best Local Similarity 56.2
Matches 18; Conservative
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US-09-853-079-211
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APPLICANT: Reed, S
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                                                                                      SEQ ID NO 211
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
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APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFREENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: EASLSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 445
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APPLICANT: Houghton, Raymond L.
APPLICANT: Bleath, Paul R.
APPLICANT: MoNeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Corist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
FILLE PERERENCE: 210121.426C11
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Pred. No. 6.7e-(
0; Mismatches
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Publication No. US20030109689A1
GENERAL INFORMATION:
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Houghton, Raymond L.
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McNeill, Patricia D.
Homer, Mary
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56.28;
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US-09-853-079-38
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US-09-737-178-38
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Best Local Similarity
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Best Local Similarity
Matches 18; Conserv
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LENGTH: 445
                                                                                                                                                                                                                                  TYPE: PRT
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APPLICANT:
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APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Meneill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Secris, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FURRENT APPLICANT 2000-12-13
CURRENT APPLICANTON NUMBER: US/09/737,178
SOFTWARE: FASTER C.
SOFTWARE: FASTER C.
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Slach, Paul R.
APPLICANT: Slach, Paul R.
APPLICANT: Moneil, Patricia D.
APPLICANT: Moneil, Patricia D.
APPLICANT: Georist, Heather
APPLICANT: Corrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT APPLICATION 105.09
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  Score 82; DB 10; Length 677;
Pred. No. 1e-08;
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Pred. No. 1.8e-08;
0; Mismatches 14
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Pred. No. 1.8e-08;
                                                                                                             931 GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 962
                                                                                     1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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                                           0; Mismatches
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                                                                                                                                                                                                                                 Sequence 87, Application US/09853079 Publication No. US20030109689A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 87, Application US/09737178 Patent No. US20010029295A1
75.9%;
56.2%;
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56.2%;
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Best Local Similarity 56.2%;
Matches 18; Conservative
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Best Local Similarity 56.28
Matches 18; Conservative
                        Best Local Similarity 56.2
Matches 18; Conservative
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US-09-853-079-87
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US-09-853-079-87
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      Query Match
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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Pauricia D.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Gorist, Heathher
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Houghton, Raymond L. APPLICANT: Sleath, Paul R. APPLICANT: Sleath, Paul R. APPLICANT: Momeill, Patricia D. APPLICANT: Homer, Mary APPLICANT: Homer, Mary APPLICANT: Homer, Mary APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION FILE REFERENCE: 210121-42611
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                      Score 82; DB 10; Length 666;
Pred. No. 1e-08;
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Pred. No. 1e-08;
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Publication No. US20030109689A1
GENERAL INFORMATION:
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Lodes, Michael J.
Houghton, Raymond L.
Sleath, Paul R.
McNeill, Patricia D.
Homer, Mary
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
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56.2%;
                                                                                                    Query Match 75.9%;
Best Local Similarity 56.2%;
Matches 18; Conservative
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Matches 18; Conservative
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APPLICANT: Reed, S
                   ; TYPE: PRT
; ORGANISM: Babesia
US-09-737-178-85
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ORGANISM: Babesia
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US-09-737-178-144
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  LENGTH: 666
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LENGTH: 677
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Gaps

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Length 32;

APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Compounds and METHODS FOR THE DIACNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIACNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REPERENCE: 210121-426611
CURRENT APPLICATION NUMBER: 05/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 32 74.1%; Score 80; DB 9; Le 100.0%; Pred. No. 1e-09; Live 0; Mismatches 0; NAME/KEY: VARIANT
LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Glutamic Acid or Alanine FEATURE: LOCATION: (3)...(3)
OTHER INFORMATION: Xaa = Glycine or Aspartic Acid LOCATION: (11)...(11)
OTHER INFORMATION: Xaa = Glutamic Acid or Glycine LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = Isoleucine or Arginine ; NAME/KEY: VARIANT ; LOCATION: (30)...(30) ; OTHER INFORMATION: Xaa = Cysteine or Histidine US-09-286-488-39 LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = Proline or Isoleucine LOCATION: (12)...(12) OTHER INFORMATION: Xaa = Lysine or Asparagine 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32 LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = Lysine or Threonine ; Sequence 39, Application US/09953079; Publication No. US20030109689A1; GENERAL INFORMATION: Query Match
Best Local Similarity 100.0
The state of the ORGANISM: Babesia microti LOCATION: (14)...(14) OTHER INFORMATION: Xaa LOCATION: (18)...(18) NAME/KEY: VARIANT US-09-853-079-39 TYPE: PRT FEATURE: FEATURE: FEATURE ò Q

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Pred. No. 1.7e-08;
0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Loughton, Raymond L.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.4263
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
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                                         NAME/KEY: VARIANT
LOCATION: (14)...(14)
LOCATION: (14)...(14)
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = Isoleucine or Arginine
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LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Glutamic Acid or Alanine
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OTHER INFORMATION: Xaa = Isoleucine or Threonine
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                                                                                                                                                                                                   LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = Histidine or Tyrosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : NAME/KEY: VARIANT
: LOCATION: (30)...(30)
: CTHER INFORMATION: Xaa = Cysteine or Histidine
US-09-737-178-39
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OTHER INFORMATION: Xaa = Threonine or Proline
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                         OTHER INFORMATION: Xaa = Lysine or Asparagine
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OTHER INFORMATION: Xaa = Cysteine or Serine
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 275
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US-09-286-488-53
Sequence 53, Application US/09286488
; Patent No. US20020169136A1
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56.28;
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Best Local Similarity 56.2
Matches 18; Conservative
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; ORGANISM: Babesia microti
US-09-286-488-53
                                                                                                                                                                                                                                              NAME/KEY: VARIANT
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILLE REFERENCE: 210.11.42669
CURRENT APPLICATION NUMBER: US/09/737,178
NUMBER OF SEQ ID NOS: 144
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o. 1e-09;
0; Indels
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OTHER INFORMATION: Xaa = Aspartic Acid or Glutamic Acid
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OTHER INFORMATION: Xaa = Glycine or Aspartic Acid
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: VARIANT
LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Glutamic Acid or Alanine
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OTHER INFORMATION: Xaa = Glutamic Acid or Glycine
NAME/KEY: VARIANT
                                                                                                                                                     LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Isoleucine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COTHER INFORMATION: Xaa = Cysteine or Histidine US-09-853-079-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = Proline or Isoleucine
OTHER INFORMATION: Xaa = Histidine or Tyrosine
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                                                             LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Threonine or Proline
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OTHER INFORMATION: Xaa = Lysine or Threonine
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                                                                                                                                                                                                                                            LOCATION: (27)...(27)
OTHER INFORMATION: Xaa - Cysteine or Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQ ID NOS: 144
FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed, Steven G.
Lodes, Michael J.
Houghton, Raymond L.
Sleath, Paul R.
MONEILL, Patricia D.
Homer, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: VARIANT
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                                           NAME/KEY: VARIANT
                                                                                                                                  NAME/KEY: VARIANT
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LENGTH: 32
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JOSTON BOOK STATE OF THE DIAGNOST SEQUENCE 53, Application US/09853079

Sequence 53, Application US/09853079

Sequence 53, Application No. US20030109689A1

GENERAL INFORMATION:

APPLICANT: Read, Steven G.

APPLICANT: Bleath, Paul R.

APPLICANT: Sleath, Paul R.

APPLICANT: Sleath, Paul R.

APPLICANT: Sleath, Paul R.

APPLICANT: Scrist, Heather

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AUMBER: US/09/853,079

CURRENT APPLICATION NUMBER: US/09/853,079

CURRENT APPLICATION NUMBER: US/09/853,079

CURRENT PELING DATE: 2010-10-09

NUMBER OF SEQ ID NOS: 224

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 53

CURRENT APPLICATION NUMBER: US/09/853,079

COBATY MATCH

SEQ ID NO 53

COBETY MATCH

SEC ID NO 54

COBETY MATCH

SEC ID NO 54

SEC ID NO 54

SEC ID NO 55

COBETY MATCH

SEC ID NO 54

SEC ID NO 54

SEC ID NO 55

COBETY MATCH

SEC ID NO 54

SEC ID NO 55

SEC ID NO
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(without alignments)
814.396 Million cell updates/sec
                                                                                                                      July 16, 2003, 17:50:14; Search time 3.7774 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                            108
1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                     283224 seqs, 96134422 residues
                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                               OM protein
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Seguence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

scrip	dextransucrase (EC cell adhesion prot cell wall-binding pseudouridine synt hypothetical prote probable caMP-depe hypothetical prote probable serine/th glutamine-fructose glutamine-fructose hypothetical prote cation cation cafius syst SCD25 protein (ver hypothetical prote inpoprotein [imported dehydrin-like prote dehydrin-like prote conserved hypothetical prote conserved hypothetical prote conserved hypothetical prote order of the protein hypothetical protein cation of hypothetical protein cation order
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A; Gene: FlyBase: Tk48D

. hypothetical prote	neurofilament trip	TTAGGG repeat-bind	hypothetical prote	hypothetical prote	transcription fact	hypothetical prote	hypothetical prote	triose-phosphate i	hypothetical prote	non intermediate f	hypothetical prote	late 33K protein -	hypothetical expor	insulin-like growt	N-acetylmuramoyl-L
2	,	53	86	33	5	, [74	5	25	25	6	7	53	17	9
A6974	OFMSI	S690	H847	S4683	A5619	T0895	G90064	S7155	G7136	T1446	T4343	S1021	F9595	A3503	C4481
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33	33	33	33	33	33	33	32	32	32	32	32	32	32	32.	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

283224

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

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C;Accession: A45866
R;Honda, O.; Kato, C.; Kuramitsu, H.K.
J. Gen. Microbiol. 136, 2099-2105, 1990
A;Title: Nucleotide sequence of the Streptococcus mutans gtfD gene encoding the gluco A;Reference number: A45866; MUID:91100958; PMID:2148600
A;Accession: A45866
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Pulido, D.; Campuzano, S.; Koda, T.; Modolell, J.; Barbacid, M.
EMBO J. 11, 391-404, 1992
A;Title: Dtrk, a Drosophila gene related to the trk family of neurotrophin receptors,
A;Feference number: S19247; MUID:92164624; PMID:1371458
A;Accession: S19247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell adhesion protein Gp160-Dtrk - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan.1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: S19247
                                                                        C;Species: Streptococcus mutans
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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A;Molecule type: mRNA
A;Residues: 1-1033 <PUL>
A;Crossreferences: EMBL:X63453; NID:97883; PIDN:CAA45053.1; PID:97884
C;Genetics:
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                                              dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans
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                                                                                                                                                                                                                                                                                                                                                                                                        hexosyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <CP4>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <CP8>
                                                                                                                                                                                                                                                                                                                                            A)Cross-references: GB:M29296
C;Superfamily: cpl repeat homology
C;Keywords: glycosyltransferase; hexosyl
F;181-201/Domain: cpl repeat homology <C
F;1127-1146/Domain: cpl repeat homology
F;1192-1211/Domain: cpl repeat homology
F;1257-1276/Domain: cpl repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;1257-1276/Domain: cpl repeat homology
F;1277-1297/Domain: cpl repeat homology
F;1321-1340/Domain: cpl repeat homology
F;1341-1361/Domain: cpl repeat homology
F;1385-1404/Domain: cpl repeat homology
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ilarity 27.6%;
Conservative 4
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Best Local Similarity
3, Conserve
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                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
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S19247
RESULT 1
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Gaps

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Length 290; 13; Indels

DB 2;

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hypothetical protein homolog MG295 - Mycoplasma genitalium C; Species: Mycoplasma genitalium 10. Sep-1999 #text_change 07-Dec-1999 (C; Accession: F64232 R; Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.M.; Firmmann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C.
Science 270, 397-403, 1995
A/Title: The minimal gene complement of Mycoplasma genitalium.
A; Reference numbor: A64200; MUID:96026346; PMID:7569993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Delius, H. submitted to the EMBL Data Library, June 1995 A;Description: 36.8 kb of S.cerevisiae chromosome XII including ACE2, CKII, PDC5, SLS A;Reference number: S59313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A;Residues: 1-251 <VER>
A;Cross-references: EMBL:273298; NID:91360532; PIDN:CAA97695.1; PID:e245566; PID:9136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:U39710; GB:L43967; NID:g1045989; PID:g1045993; TIGR:MG295 A;Experimental source: strain G-37 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Wolecule type: DNA
A;Residues: 1-367 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein YLR126c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L3105
C;Species: Saccharomyces cerevisiae
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59314; S64963; S64968; S69413
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A)Residues: 1-251 CDEL>
A)Cross-references: EMBL:X91258; NID:9995686; PIDN:CAA62637.1; PID:9995688
A)Experimental source: strain 5288C
A)Experimental source: strain 5288C
B;Verhasselt, P.; Voet, M.; Votet, M.; Octkaert, G.
submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.3%; Score 37; DB 1; Length 367; llarity 70.0%; Pred. No. 6.9; Conservative 0; Mismatches 3; Indels
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submitted to the Protein Sequence Database, May 1996
A;Reference number: S64967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Superfamily: probable membrane protein YDL033c
                                                                                                                                                   34.3%; Score 37; DB 36.4%; Pred. No. 5.4; ive 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                          79 GHPPTRANRKSVANKKKNATQT 100
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                                                                                                                                                                                                                               Conservative
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A; Accession: S64963
                                                                                                                                                       Query Match
Best Local Similarity
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nes 7; Conserv
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                                         A;Gene: VC1140
A;Map position: 1
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               C; Genetics
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Matches
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C; Species: Bacillus subtliss
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C; Accession: B65825
C; Bace: 195-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C; Accession: B65825
C; Brow, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S; Galizzi, A.; Galler, ect., J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueell
Y, M.; Ogawa, R.; Ogiwara, A.; Oudega, B.; Roche, B.; Rose, M.; Sadaie, Y.; Sacho, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tamako, T.; Terpspetra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; 
A; Cross-references: FlyBase: FBgn0004839
C; Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C; Keywords: ATP
F; 690-1028/Domain: protein kinase homology <KIN>
F; 698-706/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pseudouridine synthase family 1 protein VC1140 [imported] - Vibrio cholerae (strain N165 C;Species: Vibrio cholerae (c;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: A82236 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Ariddelberg, J.F.; Eisen, J.A.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 With the cholera pathogen Vibrio cholerae. A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . Cross-references: GB:Z99109; GB:AL009126; NID:g2633260; PIDN:CAB12776.1; PID:e1182938; Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-290 <HEI>
A;Cross-references: GB:AE004194; GB:AE003852; NID:g9655612; PIDN:AAF94299.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain NI6961; biotype El Tor
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Residues: 1-488 <KUN>
                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                               Length 1033;
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                                                                                                                                                                                                                                                                                                      11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell wall-binding protein homolog yhdD - Bacillus subtilis
                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                           Score 38.5; DB Pred. No. 9.4; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 5.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                    1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KSNSNKSSSSSSKSSNKS 166
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                                                                                                                                                                                                                               35.6%;
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ilarity 36.8%;
Conservative .:
                                                                                                                                                                                                                                                                                                      10; Conservative
                                                                                                                                                                                                                                                             Best Local Similarity
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                      Matches
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Gaps

Gaps

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Indels

Length 425

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C;Species: Caenorhabditis elegans
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C;Accession: T45654
R;Wilson, R; Ainscough, R; Anderson, K; Baynes, C; Berks, M; Bonfield, J; Burto raser, A; Fulton, L; Gardner, A; Green, P; Hawkins, T; Hillier, L; Jier, M; Jo B; O'Callaghan, M; Parsons, J; Percy, C; Rifken, L; Roopra, A; Saunders, D. Nature 368 32-38, 1994
A-Authors: Shownkeen, R; Sims, M; Smaldon, N; Smith, A; Smith, M; Sonnhammer, E. tock, L; Wilkinson-Sproat, J; Wohldman, P. A; Reference number: S43531; MUDI:9416718; PMID:7906398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: X
A;Introns: 31/3; 58/1; 279/3; 429/2; 544/3; 638/2; 801/2; 887/1; 929/2; 1025/3; 1062/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:Z68005; PIDN:CAA91990.1; GSPDB:GN00028; CESP:F59F3.1 A;Experimental source: clone F59F3 C;Genetics:
A;Residues: 1-425 <STO>
A;Cross-references: GB:AE005172; NID:g2160172; PIDN:AAB60735.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F59F3.1 - Caenorhabditis elegans .
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Y39B6B.bb [imported] - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 32.4%; Score 35; DB 2; Length 1227; Best Local Similarity 40.0%; Pred. No. 60; Matches 8; Conservative 2; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T23004
R;Kershaw, J.
submitted to the EMBL Data Library, November 1995
A;Reference number: 219651
A;Accession: T23004
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: INA
A;Residues: 1-1227 <WILD>
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                                                                                                                                             Score 35; DB 2;
Pred. No. 21;
5; Mismatches 9
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                                                                                                                                                                                                                                                                                                           | | | | : :|:| ::
197 NGNKKLDAAFRDAETKTLED 216
                                                                                                                                                                                                                                                                           6 NXNKSXXAXXKSXDTQTXQE 25
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37.5%;
                                                                                                                                                   32.4%;
30.0%;
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Best Local Similarity 30.05
Matches 6; Conservative
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Best Local Similarity 37.55
Matches 9; Conservative
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A;Note: Y39B6B.bb
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C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C; Caccession: 065132
C; Richelogis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Roneey, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A; Refrence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: C84584
R; Lin, X.; Kaul, X.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Aritle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MuID:20083487; PMID:10617197
                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-251 <VEW>
A;Cross-references: EMBL:X89514; NID:g1297019; PIDN:CAA61704.1; PID:e198755; PID:g129704
                         A;Cross-references: EMBL:273298; NID:91360532; PIDN:CAA97695.1; PID:e245566; PID:9136053
A;Experimental Source: strain S288C
R;Verhasselt, P.; Volckaert, G.
submitted to the EMBL Data Library, September 1995
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-261 <STO>
A;Cross-references: GB:AE002093; NID:94580468; PIDN:AAD24392.1; GSPDB:GN00139
C;Genetics:
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 2; Length 251;
Pred. No. 7.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 33.3%;
Best Local Similarity 32.0%;
Matches 8; Conservative
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A; Map position: 12R
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Best Local Similarity 32.33
Best Local 10; Conservative
                                                                                                                                                A; Reference number: S69393
A; Accession: S69413
A; Residues: 1-251 <DEW>
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A; Map position: 2
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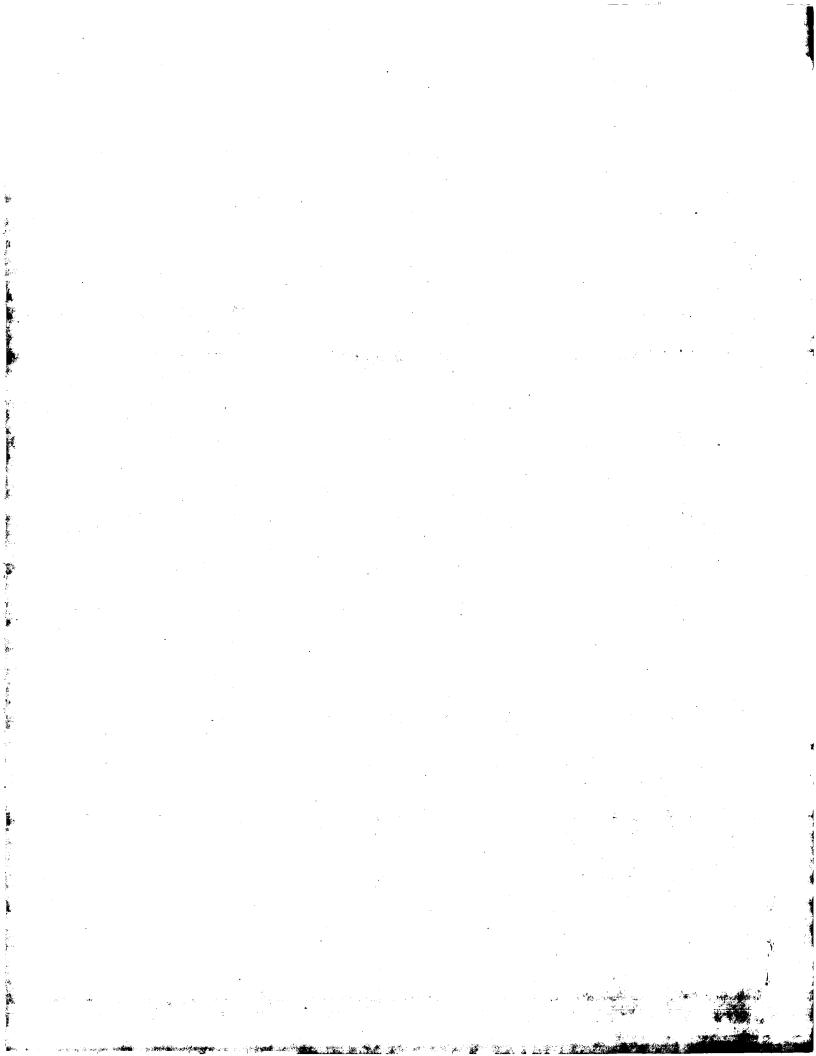
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               Gaps
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Length 82;
              Indels
               15;
DB 2;
Score 34; DB
Pred. No. 6.5;
0; Mismatches
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H71809
glutamine fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Helicobacte C; Species: Helicobacter pylori
A; Variety: strain J99
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 19-Jul-2002
C; Accession: H71809
R; Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jang, Q.; Taylor, D.E.; Vovis, G.F. Nature 397, 176-180, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Helicobacte N.Alternate names: glucosamine fructose-6-phosphate aminotransferase [misnomer] C.Species: Helicobacter pylori C.Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 19-Jul-2002 C.Accession: D64711
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A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
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submitted to the EMBL Data Library, November 1998
A;Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
A;Reference number: Z14248
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                                                                                                                                                                                       A; Residues: 1-492 <KAP>
A;Cross-references: EMBL:AC002330; NID:92262135; PID:92262143
A;Experimental source: cultivar Columbia
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                   5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB 2
Pred. No. 39;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 34; DB 2
Pred. No. 47;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | | | HEKSNPNELFIAISQSGETADTLE 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 HXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                             A,Accession: T01086
A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 YRRSNKNKSLESSSKSNHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 HXKXNXNKSXXAXXKSXDT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                31.5%;
36.8%;
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                                                                                                                                                                                                                                                                                                                                                  A;Note: T10P11.10
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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nes 7; Conserv
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D.H.; Hickey
chardson, D.;
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A:Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable serine/threonine-specific protein kinase (EC 2.7.1.-) T10P11.10 - Arabidopsis C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Mar-1999
C; Accession: T01086
R; Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la Bastide, hi, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 11-Jun-1999 #sequeuce_rolls.
C;Accession: C72250
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hichgarett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:U50308; PIDN:AAC48005.1; GSPDB:GN00023; CESP:F07C3.5 A;Experimental source: strain Bristol N2; clone F07C3 C;Genetics: A;Gene: CESP:F07C3.5
                                                                                                                                                                              hypothetical protein F07C3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Bate: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
C;Accession: T28817
R;Favello, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A;Bescription: The sequence of C. elegans cosmid F07C3.
A;Reference number: 220528
A;Reference number: 220528
A;Reference number: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Species: Thermotoga maritima
Species: Thermotoga maritima
Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
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A;Introns: 54/1; 136/1; 160/3; 210/3; 283/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F07C3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 292;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
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   4 KXNXNKSXXAXXKSXDTQTXQE 25
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4atches 7; Conservative
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Best Local Similarity
Matches 8; Conserva
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A; Residues: 1-368 <ARN>
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A; Experimental source: strain J99
C; Genetics:
A; Gene: glmS
C; Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C; Keywords: aminotransferase; intramolecular oxidoreductase; isomerase
F; 2-597/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predifF; 2/Active site: Cys #status predicted
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31.5%; Score 34; DB 2; Length 597;
Best Local Similarity 33.3%; Pred. No. 47;
Matches 8; Conservative 3; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                       2 HXKXNXNKSXXAXXKSXDTQTXQE 25 | 1 | 1 | 1 | 1 | 1 | 326 HFKSNPNELFIAISQSGETADTLE 349
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us-09-853-079-39.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:37:24 ; Search time 1.8887 Seconds (without alignments) 702.728 Million cell updates/sec Run on:

US-09-853-079-39 108 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	P49331 streptococc	P47537 mycoplasma		-	ч	026060 h glucosami	ŝ	P14771 saccharomyc	-		. P08551 mus musculu	Q02457 saccharomyc	P38700 saccharomyc			P16611 sus scrofa	P24808 bacillus su			P17936 homo sapien	Q9y7t1 schizosacch	P22059 homo sapien						P28569 saccharomyc	Q09624 caenorhabdi	P44469 haemophilus	Q9pkz4 chlamydia m	3xn9.	Q9zdi3 rickettsia
SUMMARIES	OI		TRMU_MYCGE	PODX_MOUSE	TAT_SIVA1	GLMS_HELPJ	GLMS_HELPY	YMX6_YEAST	SC25_YEAST	DHX1_ARATH	T232_BACTB	NFL_MOUSE	TBF1_YEAST	APM2_YEAST	E2F_DROME	V33P_ADE41	IBP3_PIG	CWLA_BACSU		IBP3_BOVIN	IBP3_HUMAN	YCJ5_SCHPO	OSB1_HUMAN	OSB1_RABIT	CC53_YEAST	YIN7_YEAST	MY1B_DROME	NMD2_SCHPO	TRK1_SACBA	YS89_CAEEL	PBP2_HAEIN	SSB_CHLMU	<	RS4_RICPR
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P93000 arabidopsis O91771 xenopus lae P3772 saccharomyc P38763 saccharomyc O82aw9 yersinia pe O92798 chlamydia P P47018 saccharomyc P49966 arabidopsis O75925 homo sapien P33748 saccharomyc P58363 escherichia P22763 escherichia	
GL23_ARATH HB7A_XENLA UGX2_YEAST Y112_YEAST Y0G2_YERPE Y308_CHLPN Y303_YEAST ST52_ARATH PIA1_HUMAN MSN2_YEAST ARCE_ECO57 ARCE_ECO57	
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210 220 220 223 366 444 478 478 778 778	
22 28 38 37 77 77 77 77 77 77 77 77 77 77 77 77	
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ALIGNMENTS

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01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
(EC 2.1.1.61).
                                                                                          Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                NCBI_TaxID=2097;
        TRMU_MYCGE
P47537;
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D -> Y (IN STRAIN M14251).

E -> K (IN STRAIN M14251).

G -> IR (IN STRAIN M14251).

G -> R (IN STRAIN M14251).

G -> R (IN STRAIN M14245).

Q -> H (IN STRAIN M14239).

Y -> C (IN STRAINS M14239).

Y -> C (IN STRAINS M14239).

Y -> C (IN STRAIN M14245).

N -> D (IN STRAIN M14245).

N -> D (IN STRAIN M14245).

N -> D (IN STRAINS M14245).

N -> C (IN STRAINS M14239).

N -> C (IN STRAINS M14467).

N -> C (IN STRAINS M14467).
                                                                                                                                                                                                                 S -> A (IN STRAINS MT4239, MT4245, MT4251 AND MT8148).
                                                                                       POTENTIAL.
GLUCOSYLTRANSFERASE-S.
3 X 63 AA APPROXIMATE TANDEM REPEATS.
1.
2.
3 X 7 AA APPROXIMATE TANDEM REPEATS.
3 X 7 AA APPROXIMATE TANDEM REPEATS.
4 X A APPROXIMATE TANDEM REPEATS.
5 X A APPROXIMATE TANDEM REPEATS.
5 X A APPROXIMATE TANDEM REPEATS.
7 X A A APPROXIMATE TANDEM REPEATS.
                                                                                                                                                       STRAIN MT4239 AND MT4245).
STRAINS MT4231 AND MT4148).
STRAINS MT4251 AND MT4245.
STRAINS MT4239, MT4245 AND
                                                                                                                                                                                                                                                            D -> N (IN STRAIN MT8148).
E -> D (IN STRAINS MT4239, MT4245 AND MT4251).
D -> N (IN STRAINS MT4239, MT4245 AND MT4251).
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STRAINS MT4239 AND MT4251).
STRAIN MT4239).
STRAIN MT4239, MT4251 AND
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A -> S (IN STRAIN MT4239).
TDGGSEA -> ADKGNDS (IN STRAIN MT4251)
TDGGS -> ADKGN (IN STRAINS MT4253) AND
                                                                                  Glycosyltransferase; Signal; Repeat; Dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 1462;
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W; 5C6541F0DCB0DF00 CRC64;
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| STRAIN MT4245).

| STRAIN MT4239).

| STRAIN MT8148).
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D -> N (IN S
E -> K (IN S
V -> F (IN S
F -> L (IN S
MT4467).
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Pred. No. 4
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A -> S
A -> Y
A -> V
MT8148)
EMBL, D88556; BAA26107.1; --
EMBL, D88659; BAA26111.1; --
EMBL, D88662; BAA26115.1; --
EMBL, D89979; BAA26121.1; --
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; GH_70.
Pfam; PF01473; CW_binding.1; 11.
Pfam; PF01324; Glyco_hydro_70; 1.
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27.6%;
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STRAIN-ATCC 3353 / (G-37;
STRAIN-ATCC 3353 / (G-37;
STRAIN-B-66026346; PubMed=756993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
Frim infinal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing 5-methylaminomethyl-2-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Hara T., Nakano Y., Tanaka M., Tamura K., Sekiguchi T., Minehata K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF03054; tRNA_Me_trans; 1.
TGRPAMs; TGR00420; trm0; 1.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
SEQUENCE 367 AA; 41887 MW; F8C6409D8C2D0625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3; Indels
                                                                                                                                                                                                                                                                                                                                               thiouridylate.
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE TRMU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 37; DB 1;
Pred. No. 2.6;
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15.00N-2002 (Rel. 41, Last sequence update)
15.00N-2002 (Rel. 41, Last annotation update)
Podocalyxin-like protein 1 precursor.
PODXL OR PCLP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Interpro; IPR004506; TrmU.
Interpro; IPR004135; tRNA_Me_trans.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.3%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U39709; AAC71516.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 70.0.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Q9R0M4; Q9ESZ1;
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Gaps

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17; Indels

4.2; Mismatches

Conservative

3est_Local Similarity
Matches 8; Conserv

Matches

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-!- SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
  Olmstead R.A., Hirsch V.M.;
                                                                                                                                                                                                                                                                                                          Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                    GLMS_HELPJ
                                                                                                                    KENYA.
                                                                                                                                                                                                                                                                            SEQUENCE
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                   "Identification of podocalyxin-like protein 1 as a novel cell surface marker for hemangloblasts in the murine aorta-gonad-mesonephros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                          filtration pathway between neighboring foot processes in the podocyte by charge repulsion.
SUBCELLULAR LOCATION: Type I membrane protein (Potential).
TISSUE SECTIVITY: Glomerular epithelium cell (podocyte).
PTM: Staloglycoptotein (By similarity).
SIMILARITY: BELONGS TO THE PODOCALYXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
                                                                                                                 FUNCTION: Functions as an antiadhesin that maintains an open
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
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MEDLINE-90156504; PubMed-2304139;
Johnson P.R., Fomsgaard A., Allan J., Gravell M., London W.T.,
 Copeland N.G., Jenkins N.A., Okabe M., Kogo H., Mukouyama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Indels
                                                                                Rershaw D.B., 11 J.;
"Gene structure of mouse podocalyxin.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          786A1ECF65484D1F CRC64;
                                                                                                                                                                                                                                                                                                                                         PODOCALYXIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                      Transmembrane; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAT protein (Transactivating regulatory protein).
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLCNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119 AA.
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                                                                                                                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                                                                                                                                                                                                     EMBL; AB028048; BAA86912.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          53389 MW:
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26.9%;
                                                  [mmunity 11:567-578(1999).
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                                                                                                                                                                                                                                                                                                          MGD; MGI:1351317; Podxl
                                                                                                                                                                                                                                                                                                                                        2003
2003
2003
2003
2003
1004
1007
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                                                                                                                                                                                                                                                                                                                      Signal;
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                                                               [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=11727;
                                                                                                                                                                                                                                                                                                                                                                                                                            145
154
167
206
303
78
                                                                                                                                                                                                                                                                                                                      Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1992
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                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
CARBOHYD
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                                           region.
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                                                                                                                                                                                                                                                                                                                                SIGNAL
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TAT_SIVA1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=99120557;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust T.J.,
                             unusual genetic diversity.";
J. Virol. 64:1086-1092(1990).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS-ACTIVARING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY.
GFAT SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genomic sequence comparison of two unrelated isolates of the human
'Simian immunodeficiency viruses from African green monkeys display
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GLMS OR JHP1420.
Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ranscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                         -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         !- FUNCTION: CATALYZES THE FIRST STEP IN HEXOSAMINE METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 AA; 13648 MW; 958DB1A3F7027729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31.5%; Score 34; DB 1;
41.2%; Pred. No. 3.5;
tive 2; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       596 AA.
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Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Pfam; PF00539; Tat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M29975; AAA91909.1; -
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RGRDSQTTQESQKKVEE
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Best Local Similarity
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YMX6_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ormatics and the EMBL outstation -
There are no restrictions on its
            SWISS-PROT entry is copyright. It is produced through a collaboration
                   between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (CFAU)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97394467; PubMed-9252185;
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
Teleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
McKenney K., FitzGerald L.M., Lee N., Adams M.D., Hickey E.K.,
Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
Cotton M.D., Weidman J.M., Fujii C., Bowman C., Watthey L., Wallin E.,
Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                    GATASE (BY SIMILARITY).
ISOMBRIZATION FRU-6P (BY SIMILARITY).
GLUTAMINE AMIDOTRANSFERASE.
C438BCCE6A245C28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete genome sequence of the gastric pathogen Helicobacter
                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                 Pfam; PF01380; SIS; 2.
TGRRAMS; TIGROIIS; GIMS; 1.
PROSITE; PS00443; GATASE_IYPE_II; 1.
Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                DB 1; Length 596;
                                                                                                                                                                                                                                                                                                                        13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amidotransferase) (Glucosamine-6-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                596 AA
                                                                                                                                                                                                                                                                                                                       3; Mismatches
                                                                                                                                                                                                                                                                                                Score 34;
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                                                                                                                                                                                                                                                                                                                                                                      325 HFKSNPNELFIAISOSGETADTLE 348
                                                                                                                                                                                                                                                                                                                                              2 HXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                             Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                             InterPro; IPR000583; GATase_2.
InterPro; IPR001347; SIS.
                                                                                                       EMBL; AE001564; AAD06999.1; -.
                                                                                                                                                                                                                                                                        66926 MW;
                                                                                                                                                                                                                                                                                               31.5%;
                                                                                                                                                    Pfam; PF00310; GATase_2; 1.
Pfam; PF01380; SIS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                       8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                         596 AA;
                                                                                                                     16D0
                                                                                                                                                                                                               Complete proteome.
                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                  591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID-210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GLMS OR HP1532
                                                                                                                     HSSP; P17169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helicobacter
                                                                                                                                                                                                                                                                                                                                                                                                                              GLMS_HELPY
026060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Venter J.C.
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ACT_SITE
DOMAIN
                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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between the Swiss Institute of Bioinformatics and the EMBL outstation—
the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch).
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                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
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                        SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BY SIMILARITY.
GATASE (BY SIMILARITY).
ISOMERIZATION FRU-6P (BY SIMILARITY).
GLUTAMINE AMIDOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 105.9 kDa protein in ADH3-RCAl intergenic region.
YMR086W OR YM9582.10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGRPAMS; TIGRO1135; glmS; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 1; Length 960;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gentles S., Bowman S., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: SOME, TO YEAST YKL105C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein.
SEQUENCE 960 AA; 105873 MW; 05A4FA27129DB09B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 089C534BB85AD3F1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 HFKSNPNELFIAISOSGETADTLE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
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                                                                                                                                                                                                                                                                                                                    EMBL; AE000651; AAD08570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000583; GATase_2.
InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66939 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00310; GATase_2; 1. Pfam; PF01380; SIS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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591
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nes 8; Conserv
SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete proteome.
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                                                                                                                                                                                                                                                                                                                                                                              MEROPS; C44.971;
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Q04279;
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us-09-853-079-39.rsp

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VARIANT
SEQUENCE
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                                           SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Crechet J.B., Poullet P., Mistou M.-Y., Parmeggiani A., Camonis J., Boy-Marcotte E., Damak F., Jacquet M.; "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxyl-terminal domain of SCD25."; science 248:866-868(1990).
                                                                                                                                                                                                                                                       Damak F., Boy-Marcotte E., le Roscouet D., Guilbaud R., Jacquet M.; "SDC25, a CDC25-like gene Which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae."; Mol. Cell. Biol. 11:202-212(1991).
  Gaps
                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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0
                                                                                                                                                                                                                                                                                                                                           Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M.; "The C-terminal part of a gene partially homologous to CDC 25 of suppresses the cdc25-5 mutation in Saccharomyces cerevisiae."; Gene 77:21-30(1989)
 17; Indels
                                                                                                              01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SCD25 protein.
SCD25 OR SDC25 OR YLL016W.
                                                                                             1253 AA.
 1; Mismatches
                                         438 NGNKNLENDITSSPTODLDEKSRSIEE 464
                   6 NXNKSXXAXXKSXDTQTXQEXXXXXEE
                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR: S14177; S14177.
SGD; S0003939; SDC25.
InterPro; IPR000651; RasGEFN.
InterPro; IPR001895; RasGRF_CDC25.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-91156312; PubMed-2000228;
                                                                                                                                                                                                                                                                                                                               MEDLINE-89306677; PubMed=2545538;
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 Conservative
                                                                                            STANDARD;
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                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                   STRAIN=W303
6
                                                                                            SC25_YEAST
P14771;
                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION
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                                                                                   SC25_YEAST
Matches
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A Salanoubat M., Lemcke M., Rieger M., Ansorge W., Unseld M.,
A salanoubat M., Lemcke K., Rieger M., Ansorge W., Unseld M.,
Salanoubat M., Lemcke K., Rieger M., Perez-Alonso M., Obernaier B.,
Belseny M., Boutry M., Grivell L.A., Mache R., Pulgdomench P.,
A De Simone V., Choisne N., Ariguenave F., Robert C., Brottler P.,
Rhincker P., Cattolico L., Weissenbach J., Saurin W., Ouetier F.,
Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
Nurmbach E., Drzonek H., Erile H., Jordan N., Bangert S.,
Middelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Riedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Rorad A., Hornischer K., Kauer G., Lochnert T.-H., Nordsiek G.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Reichelt J., Scharfe M., Berger-Llauro C., Purnelle B., Masuy D.,
A de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Ra Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujil C.Y., Shea T.P.,
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
euroșids II; brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                     PROSITE; PS00720; GDS_CDC25; 1.
PROSITE; PS50002; SH3; 1.
Guanine-nucleotide releasing factor; Cell cycle; Cell division;
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MEDLINE=92222990; PubMed=1623199;
Rouse D.T., Gehring C.A., Parish R.W.;
"Structure and sequence of a dehydrin-like gene in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                            DVVVKFI -> V (IN STRAIN OL136).
MW; 2DE2C9EC27E3E60D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DHX1_ARATH STANDARD; PRT; 128 AA. P25863; QS50A7; Created) 01-MAY-1992 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) MSRO1 OR DHNX OR AT3G50980 OR F24M12.20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                              POLY-ASN.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
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36.8%;
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Pfam; PF00617; RasGEF; 1.
Pfam; PF00618; RasGEFN; 1.
SMART; SM00147; RasGEF; 1.
SMART; SM00229; RasGEFN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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74
434
434
584
584
1253 AA;
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                              SM00326;
                                                                                                                                                                                                                                                          SH3 domain.
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NFL_MOUSE
P08551;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
NFL_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
             g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation-the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E., Sasamoto S., Kimura T., Idasawa K., Kawashima K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S.; Saquence and analysis of chromosome 3 of the plant Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               drought stress.
-!- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
-!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                      STRAIN=cv. Landsberg erecta; TISSUE-Leat;
MEDLINE=95035985; PubMed=7948863;
Welin B.V., Olson A., Nylander M., Palva E.T.;
"Characterization and differential expression of dhn/lea/rab-like genes during cold acclimation and drought stress in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    thaliana."; Plant Mol. Biol. 26:131-144(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacillus thuringlensis (subsp. berliner).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARG/LYS-RICH (BASIC).
HIS/LYS-RICH (BASIC).
MISSING (IN REF. 1).
983558C3E18E31F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transposase for insertion sequence element IS232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  431 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.6%; Score 33; 31.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U19537; AAB00375.1; -.
EMBL; AL132980; CAB62620.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GHHDSNKTSSLGSTTTAYDTGT 107
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MEDLINE-91072212; PubMed-2174857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00257; dehydrin; 1.
PROSITE; PS00315; DEHYDRIN_1; 1.
PROSITE; PS00823; DEHYDRIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene model prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X64199; CAA45524.1;
                                                                                                                                                                                                                                                                Nature 408:820-822(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S22485; KNMUHY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
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Les 7; Conserv
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Q99335;
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Best Local S
Matches 7
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CONFLICT
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     RRARRER RRARRE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transposition; DNA-binding; DNA recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Brain;
BELLINE-84158637; PubMed-3103856;
Julien J.-P., Meyer D., Flavell D., Hurst J., Grosveld F.;
"Cloning and developmental expression of the murine neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87064433; PubMed-3785173;
Lewis S.A., Cowan N.J.;
"Anomalous placement of introns in a member of the intermediate
filament multigene family: an evolutionary conundrum.";
Mol. Cell. Biol. 6:1529-1534(1986).
Menou G., Mahillon J., Lecadet M.-M., Lereclus D.; "Structural and genetic organization of IS232, a new insertion sequence of Bacillus thuringiensis."; J. Bacteriol. 172:6699-6696(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Last annotation update)
Neurofilament triplet L protein (68 kDa neurofilament protein)
(Neurofilament light polypeptide) (NF-L).
                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE IS21/IS408/IS1162 FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lewis S.A., Cowan N.J.; "Genetics, evolution, and expression of the 68,000-mol-wt neurofilament protein: isolation of a cloned cDNA probe."; J. Cell Biol. 100:843-850(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Indels
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431 AA; 49893 MW; 3FB218504A50767A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33;
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01-OCT-1993 (Rel. 27, Last sequ
16-OCT-2001 (Rel. 40, Last anno
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Brain Res. 387:243-250(1986).
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36.4%;
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                                                                                                                                                                                                SEQUENCE
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RESULT 12
TBF1_YEAST
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                           J. BAOL. Chem. 265:19786-19791(1990).

-1. FUNCTION: NEUROPFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.

-1. DOMAIN: THE EXTRA MASS AND HIGH CHARGE DENSITY THAT DISTINGUISH THE NEUROFILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT PROTEINS ARE DUE TO THE TAILDIECE EXTENSIONS. THIS REGION MAY FORM A CHARGED SCAFFOLDING STRUCTURE SUITABLE FOR INTERACTION WITH OTHER NEURONAL COMPONENTS OR IONS.

-1. MISCELLANGOUS: NF. L IS THE MOST ABUNDANT OF THE THREE NEURORIALAMENT PROTEINS AND, AS THE OTHER NOMEPLITHELIAL INTERMEDIATE FILAMENT PROTEINS, IT CAN FORM HOMOPOLYMERIC 10-NM
                                                  "Structure of the 68-kDa neurofilament gene and regulation of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O-LINKED (GLCNAC) (BY SIMILARITY).
O-LINKED (GLCNAC) (BY SIMILARITY).
EPITOPE (RECOGNIZED BY IF-SPECIFIC
                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
MEDLINE-91060592; PubMed-2246261;
Nakahira K., Ikenaka K., Wada K., Tamura T.A., Furuichi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 542;
Pred. No. 27;
5; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Intermediate filament; Coiled coil; Neurone; Glycoprotein. INIT_MET 0 \\ 0
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8EE9B8C6F0831D8C CRC64;
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Y -> I (IN REF. 1).
M -> K (IN REF. 1).
D -> H (IN REF. 2).
D -> H (IN REF. 1).
R -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAIL, SUBDOMAIN A.
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LINKER 12.
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LINKER 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X02165; CAB51616.1; -. EMBL; M20480; AAA39814.1; -. EMBL; M13016; AAA39810.1; -. EMBL; M55423; AAA39812.1; -.
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ilarity 25.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00038; filament; 1. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A25227; QFMSL.
MGD; MGI:97313; Nfl.
InterPro; IPR001664; IF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            239
542 AA;
                                 Mikoshiba K.;
                                                                                                                                                                                                                                                              FIT, AMENTS
                                                                 expression.";
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE STRAIN=5288C / AB972;

X MEDLINE=97313271; PubMed=9169875;

MEDLINE=97313271; PubMed=9169875;

A raujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A raujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

A raujo R., Aparicio A., Barcher M., Carpenter J., Cherry J.M.,

Chung E., Churcher C.M., Coster F., Davis R., Davis R.W.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoeft A.,

Hall J., Hebling U., Heumann R., Johnston M., Kalman S., Kleine K.,

Hall J., Hebling U., Lashkari D., Lew H., Lin D., Louis E.J.,

A Marathe R., Messenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,

A Mueller-Auer S., Namath A., Nentwich U., Oefner P., Pearson D.,

A Schremen B., Schramm S., Schroeder M., Scharfe M.,

Schreats L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,

Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

A Zhong W.W., Zollner A., Vo D.H., Hanj J.;

Nathe Dasconder M. Schreme S., Namath J.,

The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";

In Nature 387, 103-105(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: Binds the telomeric double-stranded TTAGGG repeat and negatively regulates telomere length. Involved in the regulation Essential for cell growth. May regulate gene expression. -!- SUBGUNIT: Homodimer (Probable).
                                                                                                                                                                                                                                                                                                                  Brigati C., Kurtz S., Balderes D., Vidali G., Shore D.M.;
"An essential yeast gene encoding a TTAGGG repeat-binding protein.";
Mol. Cell. Biol. 13:1306-1314(1993).
                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                         01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
TBF1 protein (TTAGGG repeat-binding factor 1) (TBF alpha).
TBF1 OR YPL128C OR LPL16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation; Cell cycle; Nuclear protein;
Chromosomal protein; Telomere; DNA-binding.
                                                                                                                                                                                          Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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DAA -> ERR (IN REF. 1).
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PIR; A48079; A48079.
HSSP, P54274; 1BA5.
TRANSFAC; T01246; -
SGD; S0006049; TBF1.
SMART; SM00395; SANT; 1.
PROSITE; PS00037; MYB_1; 1.
PROSITE; PS50090; MYB_1; 1.
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                                                                                                                                                                                                                                                                                              MEDLINE=93140769; PubMed=8423796;
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                                       01-JUL-1993 (Rel. 26, Created)
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STANDARD;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                            NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                 STRAIN-LN224
TBF1_YEAST
Q02457;
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Gaps

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Local Similarity

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Matches

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                                                                   ö
                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hilier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A late Golgi sorting function for Saccharomyces cerevisiae Apmlp, but not for Apm2p, a second yeast clathrin AP medium chain-related
                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
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                                                                   ;
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                                  Length 562;
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62823 MW; 2340F086468EC54F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                605 AA; 69990 MW; 7E216B11325EEE3C CRC64;
                                  DB 1;
28;
                                                                                                                                                                                                                                                01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
APM2 OR YHL019C.
                                                                                                                                                                                                                     605 AA
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
                                  Score 33;
Pred. No.
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Pfam; PF00928; Adap_comp_sub; 1.
PROSITE; PS00990; CLAT_ADAPTOR_M_1; 1.
PROSITE; PS00991; CLAT_ADAPTOR_M_2; 1.
                                                                                                                                                                                                                     PRT;
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MEDLINE=94378003; PubMed=8091229;
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STRAIN-S288C / REE526;
MEDLINE-95268148; PubMed-7749194;
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.. Biol. Cell 6:41-58(1995)
                                 30.6%;
53.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 265:2077-2082(1994)
                                                                                                                        | : |||| ||
516 AASATEDTQTHQE 528
                                                                                                   13 AXXKSXDTQTXQE 25
                                                                   Conservative
                                                                                                                                                                                                                     STANDARD;
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Best Local Similarity
7; Conserve
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562 AA;
                                                Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4932;
                                                                                                                                                                                                                  APM2_YEAST
P38700;
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SEQUENCE
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SEQUENCE
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Mol. Biol
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Gaps

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Indels

13;

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Pred. No.

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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandreall M.D., Zhang O., Chen L.X.,
RA Standon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxer E.G., Helf G., Melson C.R., Milklos G.L.G.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Benos P.V., Berman B.P., Bhanddari D., Botther P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellian A.E., Garraz C., Ferriacs S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garraz C., Rernisca S., Fleischmann R.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.K., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Li Z., Liang Y., Lin X.,
A Liako P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liuk K., Mattei B., McIntosh T.C., McLeod M.P., Morlherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muszhen D.R., Paceleb J.M.,
Rabason D.R., Nakolon K., Nakosken D.R., Paceleb J.M.,
Relazzolo M., Pittman G.S., Pan S., Pollard J., Pull J., P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-Oregon-R; MEDLINE-99077992; PubMed-9858578; Sasaki T., Sawado T., Yamaguchi M., Shinomiya T.; Sawaki T., Sawado T., Yamaguchi M., Shinomiya T.; Specification of regions of DNA replication initiation during embryogenesis in the 65-kilobase DNApolalpha-dE2F locus of Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dyson N.;
Drosophila E2F and DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-94158833; Pubmed-8114698;
Ohtani K., Nevins J.R.;
"Functional properties of a Drosophila homolog of the E2F1 gene.";
Mol. Cell. Biol: 14:1603-1612(1994).
                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      roc. Natl. Acad. Sci. U.S.A. 91:6359-6363(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94294381; PubMed-8022787;
Dynlacht B.D., Brook A., Dembski M., Yenush L.,
"DNA-binding and trans-activation properties of
                                                                                                                                            E2F_DROME STANDARD; PRT; 805 AA. 027368; 077035; 10-100V-1997 (Rel. 35, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) E2F OR E2F1 OR CG6376.
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|GHREHSTNKSSQYNSDEDDPNT 497
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MEDLINE-20196006; PubMed-10731132;
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Mol. Cell. Biol. 19:547-555(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rISSUE-Eye imaginal disk;
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MEDLINE=96087653; PubMed=8537434;
Hao X.F., Alphey L., Bandara L.R., Lam E.W., Glover D.,
La Thangue N.B.;
Tenotional conservation of the cell cycle-regulating transcription
of actor DRTEI/E2F and its pathway of control in Drosophila
melanogaster.";
J. Cell Sci. 108:2945-2954(1995),
L. J. Cell Sci. 108:2945-2954(1995),
C. PUNCTION: Transcriptional activator that binds to E2F sites.
Contributes to the expression of replication genes at the G1-S
Transition and Cyclin E.
C. Transition and Cyclin E.
C. Transition and Cyclin E.
C. SPECIFIC DNA BINDING AND OPTIMAL TRANS-ACTIVATION.
C. SPECIFIC DNA BINDING NUCLEAR.
C. SPECIFIC DNA BINDING NUCLEAR.
C. SPECIFICATION: Nuclear.
C. TSUB SPECIFICITY: SEgementally repeated expression throughout
C. C. SPECIFIC CLAIR SERVER SPECIFICATION NUCLEAR.
C. C. SPECIFICATION: SEGMENTALIA PREVAIL NEAR SPECIFICATION NUCLEAR SPECIFICATION NU
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodege T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zheng X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Royzman I., Whittaker A.J., Orr-Weaver T.L.;
"Mutetions in Drosophila DP and E2F distinguish G1-S progression from an associated transcriptional program.";
Genes Dev. 11:1999-2011(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duronio R.J., Bonnette P.C., O'Farrell P.H.;
"Mutations of the Drosophila dDP, dE2F, and cyclin E genes reveal
distinct roles for the E2F-DP transcription factor and cyclin E
during the G1-S translion.";
Mol. Cell. Biol. 18:141-151(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X78421; CAA55186.1; -.
EMBL; U10184; AAA19003.1; -.
EMBL; AB011813; BAA32746.1; -.
EMBL; AE001313; AAF55904.1; -.
HSSP; Q16254; ICF7.
TRANSFAC; T01547; -.
Flybase; FBgn0011766; E2F.
Flybase; FBgn003116; E2F.
Fram; PF02319; E2F.
Framscription regulation; DNA-binding; Nuclear protein;
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POLY-SER.
POLY-ASN.
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GLY-RICH.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                Gaps
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Pieniazek N.J., Velarde J.Jr., Pieniazek D., Luftig R.B.;
"Nucleotide sequence of human enteric adenovirus type 41 hexon-
associated protein VIII precursor (PVIII) including the early region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Human ademovirus type 41.
Viruses; dsDNA viruses, no RNA stage; Ademoviridae; Mastademovirus.
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MEDLINE-90272433; PubMed-2349115;
Slemenda S.B., Pieniazek N.J., Velarde J. Jr., Pieniazek D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29.6%; Score 32; DB 1; Length 217; 36.0%; Pred. No. 17;
                                                                                                                   DB 1; Length 805;
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H -> Q (IN REF. 1 AND 2).
BD49C813DDB2A77D CRC64;
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PIR; S10212; S10212.

Late protein; Phosphorylation.

SEQUENCE 217 AA; 24740 MW; B6ECDA6B3C24EC3E CRC64;
                                                                                                                                                                                                                                                                          V33P_ADE41 STANDARD; PRT; 217 AA. P19416; Q64818; Q1-NOY-1990 (Rel. 16, Created) U-NOY-1990 (Rel. 16, Last sequence update) O1-MAR-1992 (Rel. 21, Last annotation update) 33 kDa phosphoprotein.
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1; Mismatches
                                                                                                                                                2; Mismatches
                                                                                                                               41;
                                                                                                                  30.6%; Score 33; 35.0%; Pred. No. 4
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               .GLY-RICH.
POLY-GLN.
POLY-ALA.
   POLY-SER
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                                                                                      87460 MW;
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Best Local Similarity 36.v.
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805 AA;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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SMART; SM00355; Znf_C2H2; 7.
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 7.
Hypothetical protein; DNA-binding; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                               Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Primates, Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY071126; AAL48748.1; -- SEQUENCE 198 AA; 22012 MW; CE33F831FAB79D49 CRC64;
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
21nc finger protein (Hypothetical 31.0 kDa protein).
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
REI7222p.
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50.0%; Pred. No. 48;
tive 5; Mismatches
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                                                                                           Drosophila melanogaster (Fruit fly).
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EMBL; BC022842; AAH22842.1; -.
HSSP; P08046; 1A1H.
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PRINTS; PR00048; ZINCFINGER.
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Matches 9; Conserv
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Q92951;
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226 KNNINETQTSIKKV--TMTTQELCE 248
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InterPro; IPRO00569; HECT_domain.
Pfam; PF00632; HECT; 1.
SMART; SM00119; HECTC; 1.
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                                                                                                                                                                                                    Query Match 36.0%;
Best Local Similarity 47.6%;
Matches 10; Conservative
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nes 11; Conservative
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Pfam; PF00037; fer4; 1
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Q8SZ45;
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XM MEDLINE=20150912; PubMed=10688204;

XM Marchan D., Waren B.W., Moule S., Pallen M.J., Penn C.W.,

XM Maland M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,

XM Whitehead S., Barrell B.G.;

The genome sequence of the food-boine pathogen Campylobacter jejuni

The genome sequence of the food-boine pathogen Campylobacter jejuni

The genome sequence of the food-boine pathogen Campylobacter jejuni

The genome sequences.";

Nature 403:665-668(2000).

REMBL; AL139079; CAB73573.1; -

REMBL; AL130079; PRO01450; Prok_Mboxred.
                                                                                                                                                                                                                                                               Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Eisen J., Fraser C.M.;
"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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MEDLINE-J330349; PubMed-10871362;
MEDLINE-J330349; PubMed-10871362;
MITAI M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
EMBL; AE001617; AAD18480.1; -.
EMBL; AE002546; BAA988541.1; -.
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
                               Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-3UN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             923 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%; Score 50; DB 30.8%; Pred. No. 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               287 GIPNSNTLERAEKEAEKQESREQLSE 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                            pneumoniae AR39.";
Nucleic Acids Res. 28:1397-1406(2000).
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                                                                                                                                                                                                                                MEDLINE=20150255; PubMed=10684935;
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Pfam; PF01565; FAD_binding_4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 30.8%
Matches 8; Conservative
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                                                                                                                                                              SEQUENCE FROM N.A.
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   RAY REPAYED BY SECTION OF SECTION
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                                                                                                                                                                                                                    Gaps
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Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                           Length 923;
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                                                                                                                                                    Score 50; DB 16; Length 92
Pred. No. 1.2e+02;
3; Mismatches 8; Indels
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                                                            Complete proteome.
SEQUENCE 923 AA; 103909 MW; 06FC04D63259322A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U33050; AAB64910.1; -.
EMBL; D63905; BAA21482.1; -.
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT; 3268 AA.
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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%; Score 50; DB 16; Length 471; 45.5%; Pred. No. 60;
                                                                                                                                                                 Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anabaena sp. (strain PCC 7120).
Plasmid pCC7120beta.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
EMBL; APO03602: BAB77290 1; -
InterPro; IPR005094; Relaxase.
Pfam; PF03432; Relaxase; 1.
Plasmid; Hypothetical protein; Complete proteome.
Plasmid; Hypothetical protein; TDDBB895E2209G7E CRC64;
                                                                                                                           50793 MW; B38EAD4B4D0BEE6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Alr7647.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CT082 hypothetical protein.
CPN031 OR CPJ0331 OR CP0426.
Chlamydia pneumoniae (Chlamydophila pneumoniae)
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59;
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                                                                                                                                                                                                 2; Mismatches
                                                                                  TIGREAMS; TIGR01318; gltD_gamma_fam; 1.
FAD; Flavoprotein; Oxidoreductase.
SEQUENCE 465 AA; 50793 MW; B38EAD4B.
                                                                                                                                                             Score 50;
Pred. No.
   IPR000759; Adrndx_reductase.
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                    IPR001327; FAD_pyr_redox. IPR000205; NAD_binding.
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MEDLINE=21595285; Pubmed=11759840;
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MEDLINE=99206606; PubMed=10192388;
                                                                                                                                                                                                                                                         1: 1:1 | 1 | 1|1 | 1|1 | 73 NRLEEAATLSHQTNTLPEIC 92
                                                                                                                                                                                                                                    6 NKSEKAERKSHDTQTTQEIC 25
                                                                                                                                                               36.0%;
50.0%;
                                                      Pfam; PF00070; pyr_redox; 1 PRINTS; PR00419; ADXRDTASE.
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                                                                                                                                                                            l Similarity
10; Conserva
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Best Local Similarity
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   InterPro;
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Best Local 9
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Rhabditidae; Peloderinae; Caenorhabditis.
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"The gene for the Thiobacillus ferrooxidans ATCC33020 glutamate
synthase (GOGAT) small subunit complements an Escherichia coli gltD
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NCBI_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                               "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Scheet P., Gattung S.;
"The sequence of C. elegans cosmid B0261:";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases -!- COFACTOR: FAD (BY SIMILARITY).
EMBL; U36427; AAA79783.1;
                                                                                                                           ul-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Hypothetical 21.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutamate synthase small subunit gltD.
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                      2 KPNTNK---SEKAERKSHDTQTTQEI 24
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                                                                                                                                                                                                                                                                                                                                                            STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                     Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submission.";
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Best Local Similarity
Matches 10; Conserv
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STRAIN=AR39;
MEDLINE=2015055; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                              "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                                                                                                                                                                    Nucleic Acids Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                      STRAIN-J138;
MEDLINE-20330349; PubMed-10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel, 20, 01-MAR-2002 (TrEMBLrel, 20, 01-JUN-2002 (TrEMBLrel, 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AP002547; BAA98792.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 38.1
Matches 8; Conservative
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Best Local Similarity
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                         SEQUENCE FROM N.A.
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STRAIN=TLMV-NLC026;
MEDLINE=2048649; PubMed=10971131;
MEDLINE=2048649; PubMed=10971131;
This is a sequence of the sequence 
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                                                                                                                                 38.8%; Score 54; DB 3; Length 1048; 45.0%; Pred. No. 37; tive 5; Mismatches 6; Indels
                     SMART; SM00147; RasGEF; 1.
SMART; SM00229; RasGERN; 1.
PROSITE; PS00720; GDS_CDC25; 1.
SEQUENCE 1048 Aa; 121960 MW; 40alF12F9B86F458 CRC64;
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
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Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
NCBI_TaxID=83558;
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01-MAX-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILARITY to CHLPS INCA (CPJ0585 protein).
CPN0585 OR CPJ0585 OR CP0163.
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Last annotation update)
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01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2002 (TrEMBLrel. 21, Last ann
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STRAIN-CWL029;
MEDLINE-99206606; Pubmed-10192388;
                                                                                                                                                                                                                                                                     1002 PNSNSNNKSQEKSRDDQTDE 1021
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InterPro; IPR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORB1; 1'
SEQUENCE 661 AA; 78995 MW; 83C
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Best Local Similarity 45.00,
Pfam; PF00618; RasGEFN; 1.
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Neurospora crassa.
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356173; CAB91744.2; -.
InterPro; IPR000051; SAM. bind.
InterPro; IPR002792; TRAM.
InterPro; IPR001566; TrMA.
                     7EAC83171535CAB8 CRC64;
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                                                                 36.7%; Score 51; DB 16;
38.1%; Pred. No. 61;
ive 7; Mismatches 6;
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42.3%; Pred. No. 70;
tive 4; Mismatches
il protein; Complete proteome
651 AA; 75668 MW; 7EAC8317
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PROSITE; PS01230; TRMA_1; UNKNOWN_1.
PROSITE; PS01231; TRMA_2; UNKNOWN_1.
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Pfam; PF00617; RasGEF; 1.
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                                                                                  MEDLINE-20231818; PubMed-10768973;
Lodes M.J., Houghton R.L., Bruinsma B.S., Mohamath R., Reynolds L.D.,
Benson D.R., Krause P.J., Reed S.G., Persing D.H.;
"Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                          Gaps
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                                          Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia
NCBI_TaxID=5868;
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NCBI_TaxID=6239;
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                                                                                                                                                     396 AA; 44720 MW; 706E153BA5EE6B7C CRC64;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Seroreactive antigen BMN1-17 (Fragment).
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100.0%; Pred. No. 2.1e-11;
ive 0; Mismatches 0;
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Pred. No. 3.9;
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                                                                                                                    Babesia microti.";
Infect. Immun. 68:2783-2790(2000).
EMBL; AF20623.1; -.
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52.2%;
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01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Matches 12; Conservative
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tes 26; Conserv
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                                  Babesia microti
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Miosga T., Zimmermann F.K.;
"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";
Yeast 12:693-708(1996).
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MEDLINE=95348179; PubMed=7622557;
Gammie A.E., Kurihara L.J., Vallee R.B., Rose M.D.;
"DMM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";
J. Cell B.O. 130:553-566(1995).
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STRAIN=FY23 / R00053,
ARDAIN=FY23 / R00059,
MEDILINE—94375516; PubWed=8089172;
Burgess S.M., Delannoy M., Jensen R.E.;
Burgess S.M., Delannoy M., Jensen R.E.;
"MWM1 encodes a mitochondrial outer membrane protein essential for establishing and maintaining the structure of yeast mitochondria.";
J. Cell Biol. 126:1375-1391(1994).
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STRAINE-Y23 (TRD005;
MEDLINE-9087480; PubMed-1454790;
Ripmaster T.L., Vaughn G.P., Woolford J.L. Jr.;
Ripmaster T.L., vanghn G.P., Woolford J.L. Jr.;
"A putative ATP-dependent RNA helicase involved in Saccharomyces cerevisiae ribosome assembly.";
Proc. Natl. Acad. Sci. U.S.A. 89:11131-11135(1992).
                                                                                                                                                       Saccharomycetes;
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STRAIN-ALPHA S288C;
Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                                                        Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi, Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBL_TaxiD=4932;
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein L1309.
SDC25 OR SCD25 OR L1309/SCD25 OR YLL016W.
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STRAIN-FY23 /RD005;
MEDLINE-91094833; Pubmed=1986220;
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MEDLINE=96405918; PubMed=8810043;
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Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5868;
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MEDLINE-20231818; PubMed=10768973;
Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D.,
Benson D.R., Krause P.J., Reed S.G., Persing D.H.;
"Serological expression cloning of novel immunoreactive antigens of
Babesia microti.",
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275 275 WW; C3CC5D5EBC494E01 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OJ-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-2000 (TrEMBLrel. 15, Last annotation update Seroreactive antigen BMN1-20 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 139; DB 5; 100.0%; Pred. No. 1.4e-11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                             O9VWQ3
Q9R1Y9
Q9BJN1
                                                                             Q9LUN6
076734
031611
Q9VWQ6
                                                                                                                                                                                                                                                                                           Q9C551
O96137
                                                                                                                                                                                                                             Q93YZ3
Q9Z2V0
                                             Q9QYX7
Q8W191
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Q9BZT7
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015799
09NG57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Infect. Immun. 68:2783-2790(2000).
EMBL; AF206527; AAF68255.1; ...
Signal.
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SEQUENCE
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Best Local 3
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Q9NIM4;
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Q9NIM2
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Q12037 saccharomyc
Q91950 ttv-11ke mi
Q927w9 chlamydia p
Q8x093 neurospora
O01439 caenorhabdi
Q56267 thiobacillu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            003280 saccharomyc
08sz45 drosophila
092951 homo sapien
09vby9 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8zs65 anabaena sp
Q9z8k7 chlamydia p
Q9pm90 campylobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9nim2 babesia mic
Q9nim4 babesia mic
Q20227 caenorhabdi
                                                                                                                           (without alignments)
848.513 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Description
                                                                                                            July 16, 2003, 17:37:48; Search time 6.31366 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                          1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                           671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM protein - protein search, using sw model
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0901M4
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012037
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0907W9
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_unclassified:*
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sp_phage:*
sp_plant:*
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sp_archeap:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 2000000000
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Match Length
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338.5
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60.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hilbert H., Himmelreich R., Plagens H., Herrmann R.; "Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes."; Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 24:4420-4449(1996).
                                                                                                                                                                                                                                                                                                                                                     Mycoplasma pnemmoniae.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=2104;
                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL LIPOPROTEIN MPN200.
N-ACYL DIGLYCERIDE (POTENTIAL).
3E2471D7EF0A3CA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 45; DB 1; Length 798; Pred. No. 1e+02;
                                                                                                    Length 333;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                          (Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
Llipoprotein MPN200 precursor (GT9_orf798)
                                                          79 332 LYS-RICH.
333 AA; 37985 MW; 88E91737402FC4CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE000060; AAB96279.1; ...
InterPro; IPR00489; Lipoprotein_10.
InterPro; IPR004984; Lipoprotein_X.
Pfam; PR03202; Lipoprotein_10; 1.
Pfam; PF03305; Lipoprotein_10; 1.
Hypothetical protein; Lipoprotein; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Potential).
-!- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.
                                                                                                  DB 1;
                                                                                                                                                                                                                                                                  798 AA.
                                                                                                  Score 45; DB ]
Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL
            EMBL; 281035; CAB02731.1; -.
WormPep; C15H11.9; CE08186.
Ribosome biogenesis; Nuclear protein.
DOMAIN 79 332 LYS-RICH
                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-96177562; PubMed-8604303;
                                                                                                                                                           3 PNTNKSEKAERKSHDTQTTQE 23
                                                                                                                               2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23 N
87628 MW;
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ilarity 47.6%;
Conservative
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                                                                                                                                                                                                                                                                  STANDARD;
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798
                                                                                                  Query Match
Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                                                                                                                                                                                                         Hypothetical lipamph MPN200 OR MP631.
                                                                                                                                                                                                                                                               YC00_MYCPN
Q50288;
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16-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pneumoniae.
                                                                      SEQUENCE
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SORRES
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Indels

Mismatches

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9; Conservative
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P13728:
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                                                                                      SGS3_DROYA
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RRS1_CAEEL
  Matches
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          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toda H., Yazawa M., Yagi Y.;

"Amino acid sequence of calmodulin from Euglena gracilis.";

Eur. J. Biochem. 205:65-660(1992).

-!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF
ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE
CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND
PHOSPHATASES.
                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                           Length 533;
                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                      9492A18512F399CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
NCBL_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82A1E48108638455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SMART; SM00054; EFH; 4.
PROSITE; PS00018; EF_HAND; 4.
Calcium-binding; Repeat; Acetylation; Methylation.
                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                  148 AA
                                                                                                                                                                                                                                 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHYLATION.
METHYLATION.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACETYLATION
                                                                                                                     POTENTIAL. POTENTIAL.
                                                                                                                                                                                                            Score 46;
                                                                                                                                           POTENTIAL
                                                                                                                                                                  POTENTIAL
                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=2;
MEDLINE=92241300; PubMed=1572365;
                                                                                                                                                                                                                                                                           376 ESQDASTDRHDTSSNSEVCD 395
                                                                                                                                                                                                                                                      7 KSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR, JK0008; MCEG.
PIR; $21212; $21212.
HSSP; P02593; ICDM.
InterPro; IPR002048; EF-hand.
Pfam; PF00036; efhand; 4.
ProDom; PD000012; EF-hand; 2.
                                                                                                                                                                                                                                                                                                                                                      01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last seq
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                      MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16724 MW;
                                                                         EMBL; U23084; AAC49105.1; -. EMBL; 271570; CAA96212.1; -. SGD; S0005238; YNL294C. Hypothetical protein; Transme
                                                                                                                                                                                                           33.1%;
35.0%;
                                                                                                                                                                                                                      Best_Local Similarity 35.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                           protein; T.
95 115
128 148
179 199
                                                                                                                                          179
210
248
281
533 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                 Euglena gracilis.
                                                                                                                                                                                                                                                                                                                                                                 01-JUL-1989 (
30-MAY-2000 (
Calmodulin.
                                                                                                                                                                                                                                                                                                                              CALM_EUGGR
P11118;
                                                                                                                                                                          TRANSMEM
SEQUENCE
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SEQUENCE
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                                                                                                                       TRANSMEM
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Length 148;

Score 45; DB 1; Pred. No. 19;

32.48; 64.38;

Best Local Similarity

Query Match

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                                                                                                                                                                                                                                                                                                                               Hexapoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-88332966; PubMed-3138416; Martin C.H., Mayeda C.A., Meyerowitz E.M.; Martin C.H., Mayeda C.A., Meyerowitz E.M.; Martin C.H., Mayeda C.A., Meyerowitz E.M.; J. Mol. Biol. 201:273-287(1988).
J. Mol. Biol. 201:273-287(1988).
J. Holl ELOPMENTAL STAGE: PRODUCED BY THIRD-INSTAR LARVAE.
PIR: $01360; $01360.
FlyBase; FBGn0013172; Dyak\S9s3.
                                                                                                                                                                                                                                                                                                    Drosophila yakuba (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapo
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroldea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bardill S.C.;
Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Involved in ribosome biogenesis (By similarity).
-!- SUBCELCULAR LOCATION: Nuclear (By similarity).
-!- SIBCELCULAR LOCATION: Nuclear (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 45; DB 1; Length 263;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SALIVARY GLUE PROTEIN SGS-3.
C0C5246B482A261C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribosome biogenesis regulatory protein homolog
                                                                                                                                                                                            01-JAN-1990 (Rel. 13, Created)
10-A02-1991 (Rel. 19, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Salivary glue protein Sgs-3 precursor.
                                                                                                                                                        263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      333 AA.
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6; Mismatches
                                                                                                                                                     PRT;
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HTTKSTTSKRPTHETTTSK 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23
263 SP
28392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.00,
Best Local Similarity 40.00,
                                                                                                                                                        STANDARD;
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13 RKSHDTQTTQEICE
                                        74 RKMHDTDTEEIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nilges M., Macias M.J., O'Donoghue S.I., Oschkinat H., antiomated NOESY interpretation with ambiguous distance restraints: the refined NMR solution structure of the pleckstrin homology domain
                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
115-JUN-2002 (Rel. 41, Last annotation update)
Spectrin beta chain, brain 1 (Spectrin, non-erythroid beta chain 1)
(Beta-11 spectrin) (Fodin beta chain).
SPTBNI OR SPTB2 OR SPNB2 OR SPNB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 14:4676-4681(1995).

-!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
THUS CANDIDATE FOR THE CALCUIM-DEPENDENT MOVEMENT OF THE
CYTOSKELETON AT THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                  'Structure of the pleckstrin homology domain from beta-spectrin.";
                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                           STRAIN=BALB/C;
MEDLINE-93340985; PubMed-8479293;
MA Y., Zimmer W.E., Riederer B.M., Goodman S.R.;
"The complete anino acid sequence for brain beta spectrin (beta fodrin): relationship to globin sequences.";
Brain Res. Mol. Brain Res. 18:87-89(1993).
                                                                                                                                                                                                                                                                                                                                                                                                    Macias M.J., Musacchio A., Ponstingl H., Nilges M., Saraste M.,
Oschkinat H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Structure of the binding site for inositol phosphates in a PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hyvoenen M., Macias M.J., Nilges M., Oschkinat H., Saraste M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -:- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
-:- SIMILARITY: CONTAINS 2 CALPONIN-HOWOLOGY (CH) DOMAINS.
-:- SIMILARITY: CONTAINS 1 PH DOMAIN.
-:- SIMILARITY: CONTAINS 1 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2199-2304. MEDLINE=96030773; PubMed=7588597;
                                           PRT; 2363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:98388; Spnb2.
Interpro; IPR001589; Actbind_actnin.
Interpro; IPR001715; Calponin-like.
Interpro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-94268558; PubMed-8208297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97342712; PubMed-9199409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from beta-spectrin.";
J. Mol. Biol. 269:408-422(1997).
                                                                                                                                                                                                                                                                                                                                                                        STRUCTURE BY NMR OF 2199-2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRUCTURE BY NMR OF 2199-2304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M74773; AAC42040.1; -. PDB; 1BTN; 08-MAR-96. PDB; 1MPH; 16-JUN-97.
                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 369:675-677(1994).
                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
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                                           SPCO_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      domain.";
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MEDLINE=5613033; PubMed=8553702;
MEDLINE=9613033; PubMed=8553702;
MEDLINE=9613033; PubMed=8553702;
MEDLINE=9613033; PubMed=8553702;
"Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and a novel putative serine/threonine protein kinase gene.";
Teast 11:1303-1310(1995).
-: SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                        ### PF00169; PH; 1.
Pfam; PF00307; CH; 2.
Pfam; PF00307; CH; 2.
Pfam; PF00435; Spectrin; 18.
PRINTS; PR00603; SPECTRINPH.
SMART; SM00033; CH; 2.
SMART; SM00150; PEC; 16.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00021; CH; 2.
PROSITE; PS500031; CH; 2.
PROSITE; PS500031; CH; 2.
CYLOSKeleton; Membrane; Repeat; Actin-binding; Capping protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; o .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 61.5 KDa protein in CLA4-PUS4 intergenic region.
                                                                                                                                                                                                 ACTIN-BINDING (BY SIMILARITY).
CH 1.
CH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 47; DB 1; Length 2363; Pred. No. 1.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274420 MW; 64C9E4BD26BBC7B8 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              533 AA
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                                                                                                                                                                                                                                                                                  SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
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SPECTRIN 17
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                IPR001605; Spectrin_PH.
InterPro; IPR002017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33.8%;
37.5%;
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1775
1881
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1988 21:
2196 23:
2363 AA;
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Best Local Similarity
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                                                                                                                                                                                                                     3D-structure.
DOMAIN
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P48565;
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SEQUENCE
                  InterPro
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49 NKSEKEENKIHDDRRVE 65
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Matches 9; Conserv
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                                                                                                                                                                                         Core protein.
SEQUENCE 36
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                                                                                                                                                                                                                                                                                                                                                 VP6_AHSV6
Q64913:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MSPSGRLCLITIVGLILPTRGGTLKDTTSSSSADSTIMDIO
VPTRAPDAVYTBLQPTSPTPTWPADETPQPQTGTQQLEGTD
GPLVTDPETHKSTKA -> MQTLSNIPCFCLHGSLLPSTDL
ATLS (IN ISOFORM 2).
                                                                                    Omasa T., Chen Y.G., Mantalaris A., Wu J.H.D.;
"A cDNA from human bone marrow encoding a protein exhibiting homology
to the ATPIL/PDM/MAT8 family of transmembrane proteins.";
Blochim. Biophys. Acta 1517:307-310(2001).
-: SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-: SIMILARITY: BELONGS TO THE FXYD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            African horse sickness virus 3 (AHSV-3) (African horse sickness virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9; Indels
                             Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IN DBSNP:1688005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7429D5A838B75AA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                     PROSITE; PRO1310; FXYD; 1.
Transmembrane; Signal; Ionic channel; Ion transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /FTId=VAR_012349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> SH (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (serotype 3)).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VP6 protein (Minor inner core protein VP6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  369 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
                                                                                                                                                                                                                                                                                                              InterPro; IPR000272; ATP1G1_PLM_MAT8.
                                                               TISSUE-Bone marrow;
MEDLINE-21240216; PubMed-11342114;
                                                                                                                                                                                                                                                                                                                                                        Alternative splicing; Polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 PETHKSTKAAHPTDDTTTLSE 109
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                                                      SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                      EMBL; AF161462; AAF29077.1; -. EMBL; BC009642; AAH09642.1; -. EMBL; AF177940; AAG09301.1; -.
SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Rel. 37, Created)
(Rel. 37, Last sequ
(Rel. 37, Last anno
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164
178
97
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178
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178 AA;
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           ISSUE-Pancreas;
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                    Strausberg R.
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Q64909;
15-DEC-1998 (
15-DEC-1998 (
15-DEC-1998 (
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TRANSMEM
DOMAIN
VARSPLIC
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                                                                                                                                                                                                                                                                                         Genew;
                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   African horse sickness virus 6 (AHSV-6) (African horse sickness virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
Turnbull P.J., Cormack S.B., Huismans H.; "Characterization of the gene encoding core protein VP6 of two African horsesickness virus serotypes."; J. Gen. Virol. 77:1421-1423(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96335674; PubMed=8757982;
Turnbull P.J., Cormack S.B., Huismans H.;
"Characterization of the gene encoding core protein VP6 of two
African horsesickness virus serotypes.";
J. Gen. Virol. 77:1421-1423(1996).
-! SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 47; DB 1; Length 369;
pred. No. 25;
2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.8%; Score 47; DB 1; Length 369; 52.9%; Pred. No. 25; ive 2; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AA; 38464 MW; E696B1EF41A92768 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AA; 38450 MW; 1ECFCCOFFFF21FE9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
1-DEC-1998 (Rel. 37, Last annotation update)
UP6 protein (Minor inner core protein VP6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (serotype 6)).
Viruses; dsRNA viruses; Reoviridae; Orbivirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U33000; AAB17107.1; -.
InterPro; IPR001399; Orbi_VP6.
Pfam; PF01516; Orbi_VP6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001399; Orbi_VP6.
Pfam; PF01516; Orbi_VP6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NKSEKAERKSHDTQTTQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 NKSEKEENKIHDDRRVE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 NKSEKAERKSHDTQTTQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.8%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U19881; AAB17103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guery Match
Best Local Similarity 52.57
Best Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
         Theologis A., Ecker J.R., Palmo, J., Federspiel N.A., Kaul S.,
A Mite O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
Buehler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Cond L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
Chung M.K., Cold M.L., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
A. Gill J.E., Johnson Hopson C., Khan S., Khaykin E.,
A. Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,
Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
A. Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,
A. Milscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
A. Wu D., Yu G., Fraser C.M., Vasberg M., Vysotskaia V.S., Walker M.,
T., Saguence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                     FUNCTION: CENTRAL COMPONENT OF THE RECEPTOR COMPLEX RESPONSIBLE FOR THE RECGENTION AND TRANSLOCATION OF CYTOSOLICALLY SYNTHESIZED MITOCHONDRIAL PREPROTEINS. TOGETHER WITH TOWAZ PROTIONS AS THE TRANSIT PEPTIDE RECEPTOR AT THE SURFACE OF THE MITOCHONDRION OUTER MEMBRANE AND FACILITATES THE MOVEMENT OF PREPROTEINS INTO
                                                                                                                                                                                                                                                                                                                                                                                                                    PTM: THE N-TERMINUS IS BLOCKED.
MISCELLANEOUS: THERE ARE FOUR GENES (TOM20-1, TOM20-2, TOM20-3 AND TOM20-4) WHICH ENCODE MITOCHONDRIAL IMPORT RECEPTOR SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                            SUBUNIT: FORMS PART OF MITOCHONDRIAL RECEPTOR COMPLEX. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35.3%; Score 49; DB 1; Length 210; 28.0%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thyroid receptor interacting protein 7 (TRIP7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F -> L (IN REF. 2).
MISSING (IN REF. 2).
65EA3327249A62E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE TOM20 FAMILY.
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MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ296024; CAC14429.1; -. EMBL; AC004557; AAF99745.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23204 MW;
                                                                                                                                                                                                                                                                                                                                                               THE TRANSLOCATION PORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7; Conservative
                                                                                                                                                                                                                                                                        Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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199
210
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                                                                                                                                                                                                                                                                                                                                                                                                         outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210 AA;
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11
168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRI7_HUMAN
Q15651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                       MOI. Endocrinol. 9:243-254(1995).
-1- FUNCTION: INTERFACTS, IN VITRO, WITH THE LIGAND BINDING DOMAIN OF
THE THYROLD RECEPTOR (TR). TRIP? REQUIRES THE PRESENCE OF THYROLD
HORMONE FOR ITS INTERACTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear.
-!- TISSUE SPECIFICITY: ABUNDARLY EXPRESSED IN KIDNEY, SKELETAL
MUSCLE AND HEART. LOWER LEVELS FOUND IN LUNG, LIVER AND PANCREAS.
-!- SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY.
                                                                                                                                                                                                           Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; "Two classes of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

FXXD domain-containing ion transport regulator 5 precursor

(Dysadherin) (HSPC113).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.8%; Score 47; DB 1; Length 120; 37.5%; Pred. No. 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 120 AA; 13016 MW; 2B7A0B9D352BF78F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               178 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000079; Highmoblty_14_17.
Pfam; PF01101; HMG14_17; 1.
SMART; SM00527; HMG14_17; 1.
PROSITE: PS00355; HMG14_17; 1.
Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKPNTNKSEKAERKSHDTQTTQEI 24
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                                                                                                                                                                         MEDLINE-95295737; PubMed-7776974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      stem/progenitor cells.";
Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; L40357; AAA73877.1; -. Genew; HGNC:12312; TRIP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 37,32
Best Local Similarity 37,32
Source 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
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                                                                                                                                    SEQUENCE FROM N.A.
                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
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SEQUENCE FROM N.A. STRAIN=cv. Columbia;
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SEQUENCE
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OM22_ARATH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                   Oncogene 6:347-349(1991).
-!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
-!- MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES CAME LEVEL) NO HAS SIMILAR FUNCTIONS AS CDC25.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
"The COOH-domain of the product of the Saccharomyces cerevisiae gene elicits activation of p21-ras proteins in mammalian cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Guanine-nucleotide releasing factor; Cell cycle; Cell division;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-Bristol N2;
MEDLINE-9728461; PubMed-9136770;
Twasaki K., Staunton J., Saifee O., Nonet M., Thomas J.H.;
"aex-3 encodes a novel regulator of presynaptic activity in C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10 DVVVKFI -> V (IN STRAIN 0L136).
144979 MW; 2DE2C9EC27E3E60D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 54; DB 1; Length 1253;
Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AEX3_CAEEL STANDARD; PRT; 1409 AA. 002626; 027467; 1409 AA. 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last sequence update) 16-007-2001 (Rel. 40, Last annotation update) Regulator of presynaptic activity aex-3. Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5; Mismatches
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POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                              PIR: S14177; S14177.
SGD: S0003939; SDC25.
InterPro: IPR000651; RasGEFN.
InterPro: IPR001895; RasGRF_CDC25.
InterPro: IPR001495; SH3.
Ffam: PF00618; SH3.
Pfam: PF00618; RasGEFN: 1.
Pfam: PF00618; RasGEFN: 1.
SWART: SW00229; RasGEFN: 1.
SWART: SW00229; SH3: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 PNTNKSEKAERKSHDTQTTQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00720; GDS_CDC25; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                EMBL; M26647; AAA16565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.8%;
45.0%;
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79
437
590
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74 7
434 43
584 59
1253 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SH3 domain.
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                               in synaptic transmission.";
EMBO 0.1 19.4806-4816(2000).
-!- FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) FOR RAB3. MAY
REGULATE TWO DIFFERENT PATHWAYS FOR NEURAL ACTIVITIES.
                                                             INTERACTION WITH CAB-1.
MEDILINE-2014846; PubMed=10970871;
Hasaaki K., Toyonaga R.;
"The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OM22_ARATH STANDARD; PRT; 210 AA.
P82873; OSFZJ6;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mitochondrial import receptor subunit TOM20-2 (Translocase of outer membrane 20 kpa subunit 2).
TOM20-2 OR ATIG27390 OR F17L21.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Purification and characterization of the preprotein translocase of the outer mitochondrial membrane from Arabidopsis thaliana. Identification of multiple forms of TOM20."; Plant Physiol. 125:943-954(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 50; DB 1; Length 1409;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                          -i- SUBUNIT: BINDS TO CAB-1.
-i- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS.
-i- SIMILARITY: CONTAINS 1 DENN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 SER-RICH.
157458 MW; 2DDE6395AC963313 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10; Indels
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 39; 7; Mismatches
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InterPro; IPR001194; DENN.
InterPro; IPR005112; dDENN.
InterPro; IPR005113; uDENN.
Pfam; PF02141; DENN; 1.
Pfam; PF03455; dDENN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U49945; AAC47926.1; -.
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PubMed=11161051;
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us-09-853-079-195.rsp

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crechet J.B., Poullet P., Mistou M.-Y., Parmeggiani A., Camonis J., Boy-Marcotte E., Damak F., Jacquet M.; "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxyl-terminal domain of SCD25."; Science 248:866-868(1990).
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91094833; PubMed=1986220; Damak F., Boy-Warcotte E., le Roscouet D., Guilbaud R., Jacquet M.; SDC25, a CDC25-like gene which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae."; Mol. Cell. Biol. 11:202-212(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rey I., Schweighoffer F., Barlat I., Camonis J., Boy-Marcotte E.,
Gullbaud R., Jacquet M., Tocque B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1158;
                                                                                                                                                                                                                                               Transcription regulation, Nuclear protein.

CONFLICT 124 124 P -> R (IN REF. 1).

CONFLICT 448 448 R -> G (IN REF. 1).

CONFLICT 721 726 NKGKSE -> TKGRVK (IN REF. 1).

CONFLICT 1080 1080 T -> A (IN REF. 1).

SEQUENCE 1158 AA; 126941 MW; 81FC424968E9A5F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
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15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                 Score 54; DB Pred. No. 9; 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        718 GNPNKGKSEKKEKTPLRDESTQEHSE 743
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                                                                                                                                                              EMBL; AF248484; AAF62185.1; -. EMBL; AF127577; AAF35255.1; -. EMBL; AL163207; CAB90396.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 668-1253 FROM N.A.
                                                                                                                                                 EMBL; X84373; CAA59108.1; -.
                                                                                                                                                                                                                                                                                                                                                                 38.8%;
46.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCD25 protein.
SCD25 OR SDC25 OR YLL016W.
                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                HGNC:8001; NRIP1.
                                                                                                                                                                                                                                                                                                                                                                                 12; Conserv
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                                                                                                                                                                                                                                     MIM; 602490; -.
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P14771;
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Best Local
                                                                                                                                                                                                                   Genew;
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Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Reichwald K., Rump A., Schillabel M., Schudy A., Zimmermann W.,
Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Webinneyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                R InterPro; Iranoway;

R Pfam; PR00545; DnaJ_CXXCXGXG; 1.

R Pfam; PR00545; DnaJ_CXXCXGXG; 1.

R PRINTS; PR00525; DnaJ_C; 1.

R RINTS; PR00521; DnaJ_CX; 1.

R RNSITE; PS00637; DNAJ_CXXCXGXG; 1.

DR PROSITE; PS00637; DNAJ_CXXCXGXG; 1.

DR PROSITE; PS00765; DNAJ_CXXCXGXG; 1.

RW Chaperone; Heat shock; Mitochondrion; Repeat; Transit peptide.

FT FRANSIT 1 55 MITOCHONDRION (POTENTIAL).

FT FRANSIT 56 511 MDJ1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cavailles V., Dauvois S., L'Horset F., Lopez G., Hoare S.,
Kushner P.J., Parker M.G.;
"Nuclear factor RIP140 modulates transcriptional activation by the estrogen receptor."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- FUNCTION: MODULATES TRANSCRIPTIONAL ACTIVATION BY THE ESTROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nuclear factor RIP140 (Nuclear receptor interacting protein 1).
                                                                                                                                                                                                                                                                                                                                                                Length 511;
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                                                                                                                                                                                                                                                                                                                                 007343427C66D2B6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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Last annotation update)
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CXXCXGXG MOTIF
CXXCXGXG MOTIF
CXXCXGXG MOTIF
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"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                 Score 56; DB :
Pred. No. 2.1;
2; Mismatches
                                                                                                                                                                                                                              J-DOMAIN.
GLY-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001:305; DnaJ_CXXCXGXG.
IPR001623; DnaJ_N.
IPR003095; HSp_DnaJ.
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MEDLINE=95369246; PubMed=7641693;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                 55561 MW;
                                                                                                                                                                                                                                                                                                                                                                40.3%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 14:3741-3751(1995).
                                                                                                                                                                                                                                                                                                                                                                                                  11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                               127
186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel. 33, (Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                               511 AA;
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
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SEQUENCE FROM N.A.
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16-OCT-2001
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P48552;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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DOMAIN
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us-09-853-079-195.rsp

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:37:24; Search time 1.53457 Seconds (without alignments) 702.728 Million cell updates/sec Run on:

Title:

US-09-853-079-195 139 1 GKPNTNKSEKAERKSHDTQTTQEICE 26 Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

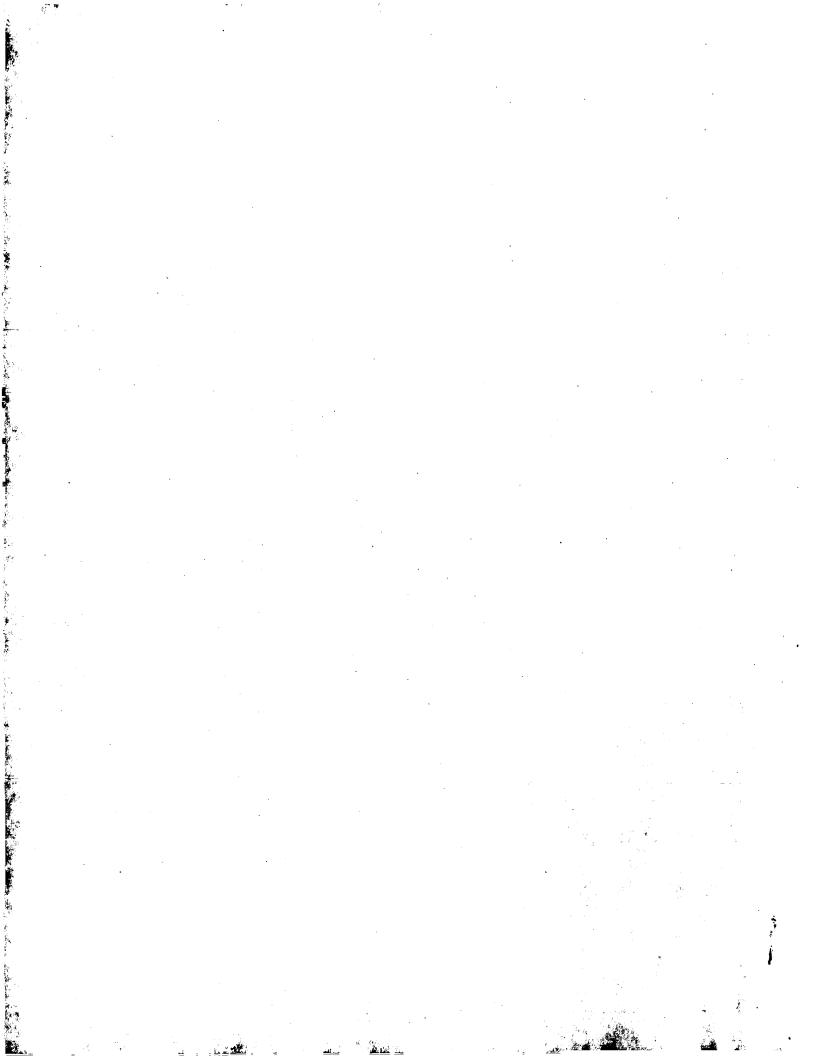
Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	P35.91 Saccharowyc P4855 homo sapien P14771 Saccharowyc O02626 caenorhabdi P82873 arabidopsis O15651 homo sapien Q64909 african hor Q64913 african hor Q64913 african hor Q64913 african hor Q62261 mus musculu P4855 saccharowyc P11118 euglana gra P13728 drosophila Q9xvt Ocaenorhabdi Q50508 mycoplasma Q65050 saccharowyc P98175 homo sapien P12036 homo sapien P49452 mus musculu P49228 deinococcus Q63328 bluetcongue Q9qund mus musculu P4928 deinococcus Q63328 bluetcongue Q9qund mus musculu Q60164 schizosacch P76238 mycoplasma Q9pc95 xylella fas P09141 photobacter P87126 schizosacch Q9und homo sapien Q9pund homo sapien
SUMMARIES	MDJ1_YEAST R114_HUMAN SC25_TRAST AEX3_CAREL OM22_ARATH FYR5_HUMAN VP6_AHSV3 VP6_AHSV3 VP6_AHSV3 VP6_AHSV3 VP6_AHSV3 VP6_AHSV3 VP6_AHSV4 VP6_AHSV3 VP6_AHSV3 VP6_AHSV4 VP6_AHSV4 VP6_AHSV4 VP6_AHSV4 VP6_AHSV5 VP6_AHSV6 VP6_AHSV6 VP6_AHSV6 VP6_AHSV6 VP6_AHSV6 VP6_AHSV6 VP6_AHSV6 VP6_AHSV6 VP6_AHSV7 VP6_BTV1S
DB	
Length	11111 112093 11200 12100 12100 12003 13003 13003 1020 1020
% Query Match	33.0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0
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Submitted to the EMBL Data Library, August 1995
A; Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.
A; Reference number: 869554
A; Accession: 859625
A; Molecule type: DNA
A; Residues: 1-3268 <DIE>
A; Residues: 1-3268 <DIE>
A; Cross-references: EMBL: U33050; NID: 9927726; PIDN: AAB64910.1; PID: 9927738; MIPS: YDR457x
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40036
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-803 <WOO>
A;Cross-references: EMBL:AL021766; PIDN:CAA16907.1; GSPDB:GN00067; SPDB:SPBC27B12.12c
A;Experimental source: strain 972h-; cosmid c27B12
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hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001
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Pred. No. 1.6e+02;
6; Mismatches 6; Indels
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Pred. No. 56;
5; Mismatches
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A;Cross-references: SGD:S0002865; MIPS:YDR457w
A;Map position: 4R
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34.8%;
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Best Local Similarity 44.0%;
Matches 11; Conservative
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Best Local Similarity 34.8<sup>th</sup>
Matches 8; Conservative
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A.Gene: SPDB:SPBC27B12.12c
A.Map position: 2
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                                                                             Accession: $69625
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Gaps

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Indels

Length 579;

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Cyaccession: G8123
Ryparkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill
C.W.; Ouail, W. Ryajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar
Nature 403, 665-668, 2000
A; Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A; Reference number: A81250; MUD:20150912; PMID:10688204
A; Accession: G81253
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-923 < PAR>
A; Cross-references: GB:AL139079; GB:AL11168; NID:g6968971; PIDN:CAB73573.1; PID:g696
A; Experimental source: serotype 02, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Introns: 77/1; 136/2; 183/2; 232/3; 283/3; 386/3; 427/3; 527/3; 577/1; 699/3; 782/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable oxidoreductase Cil585c [imported] - Campylobacter jejuni (strain NCTC 11168) C;Species: Campylobacter jejuni C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     presynaptic activity regulator aex-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 1409; 71;
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R:Leimbac, D.: Minx, M.
Submitted to the EMBL Data Library, February 1996
A:Description: The Sequence of C. elegans cosmid C02H7.
A:Reference number: 220523
A:Reference number: 220523
A:Reference number: 220523
A:Reference number: 240523
A:Reference number: 220523
A:Reference number: 220523
A:Reference number: 220523
A:Residues: 1-1409
A:Residues: 1-1409
A:Residues: 1-1409
A:Cross-references: EMBL:U49945; PIDN:AAC47926.1; GSPDB:GN00029
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Pred. No. 46;
3; Mismatches
                                                                                                                              ; Score 50; DB 2;
; Pred. No. 29;
10; Mismatches
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30.8%;
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Best Local Similarity 47.6%;
Matches 10; Conservative
                                                                                     Query Match
Best Local Similarity 30.00
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Matches 8; Conserv
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    C;Genetics:
A;Gene: CPj0331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A.Cross-references: GB.AE001617; GB.AE001363; NID:q4376599; PIDN:AAD18480.1; PID:g437666 A.Experimental Source: strain CWL029 R.VE40 R. Read. T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000 A.TILLE: Genome sequences of Chlamydia trachomatis Mopn and Chlamydia pneumoniae AR39. A.Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Residues: 1-579 <REA>
A;Cross-references: GB:AE002204; GB:AE002161; NID:g7189350; PIDN:AAF38269.1; PID:g718935
C;Genetics:
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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: D72092
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A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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                                    A; Residues: 1-471 <KUR>
A; Cross-references: GB:AP003602; PIDN:BAB77290.1; PID:g17134732; GSPDB:GN00181
A; Experimental source: strain PCC 7120
C; Genetics: A; 
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A;Residues: 1-579 <STO>
A;Cross-references: GB:BA000008; NID:g8978705; PIDN:BAA98541.1; GSPDB:GN00142
A;Experimental source: strain J138
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29;
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Pred. No. 24;
4; Mismatches
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30.8%; Pred. No. 29;
live 10; Mismatches
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Best Local Similarity
Matches 8; Conserv
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Best Local Similarity
Matches 10; Conserv
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A; Molecule type: DNA
A; Residues: 1-579 <ARN>
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A; Molecule type: DNA
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C; Species: Nostoc sp.
A;Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C;Accession: AD2545
R;Rancko, T:, Nakamura, Y:; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Accession: JC5184
R. Deane, S. M.; Rawlings, D. E.
Gene 177, 261-263, 1996
A. Title: Cloning and sequencing of the gene for the Thiobacillus ferrooxidans ATCC330
A. Reference number: JC5184; MUID: 97080532; PMID: 8921877
A. Accession: JC5184
A. Status: preliminary; nucleic acid sequence not shown
A. Molecule type: DNA
A. Residues: 1-465 < DEA>
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F;151-156,291-256/Region: glycine-rich
F;427-437/Region: FAD-binding #status predicted
F;457-437/Region: FAD-binding #status iron-sulfur clusters (Cys) (covalent) #stat
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                                                                                                                                                                                                                                                                 A; Residues: 1-196 <SCH>
A; Cross-references: EMBL:U97016; PIDN:AAB52352.1; GSPDB:GN00019; CESP:B0261.5
A; Experimental source: strain Bristol N2; clone B0261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C.Species: Thiobacillus ferrooxidans
C.Date: 16-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 29-Sep-1999
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:U36427; NID:91033069; PIDN:AAA79783.1; PID:91033071
A;Experimental source: strain ATCC33020
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                                                                                     Library, April 1997
s of C. elegans cosmid B0261
                                                                                                                                                                                                       A; Status: preliminary; translated from GB/EMBL/DDBJ
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2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 50;
Pred. No.
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                                                                                                                    A; Description: The sequence of C.
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43.5%;
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Matches 10; Conservative
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                                                       R;Scheet, P.; Gattung, S. submitted to the EMBL Data
                                                                                                                                                  A; Reference number: 220036
A; Accession: T25445
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Best Local Similarity
Matches 10; Conserv
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A;Introns: 162/3
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                                                                                                                                      C; Species: Chianydophila pneumoniae, Chlanydia pneumoniae (Schaff 1920)
C; Species: Chianydophila pneumoniae, Chlanydia pneumoniae
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
C; Accession: F86563
R; Shirai, M.; Hirakava, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID:20330349; PMID:10871362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein CP0163 [imported] - Chlamydophila pneumoniae (strains CWL029 and AR N:Alternate names: hypothetical protein CPn0585 C;Species: Chlamydophila pneumoniae, Chlamydiap neumoniae, Chlamydiap sequence_revision 23-Apr-1999 #text_change 11-May-2000 C;Accession: A72060; B81607
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A.Experimental source: strain CWL029
R.Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
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A;Experimental source: strain AR39, HL cells
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As Title: Comparative genemes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                                 hypothetical protein CPj0585 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001
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Pred. No. 24;
7; Mismatches
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Pred. No.
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38.1%;
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38.1%;
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Best Local Similarity
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Best Local Similarity
Matches 8; Conserv
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A;Molecule type: DNA
A;Residues: 1-651 <REA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Experimental source: C:Genetics:
A:Gene: CPn0585; CP0163
                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Accession: B81607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CPj0585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    270
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Saccharomyces cerevisiae on a 43.7

of

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Gaps

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Indels

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Length 1048;

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A;Molecule type: DNA
A;Residues: 1-1048 <MIW>
A;Cross-references: EMBL:X91488; NID:g1495203; PIDN:CAA62775.1; PID:g1495207
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: CDC25-type guanine nucleotide exchange activator homology F;744-995/Domain: CDC25-type guanine nucleotide exchange activator homology
         A; Cross-references: EMBL: X97560; NID: g1297003; PID: e238680; PID: g1297014
                                                                                                                                                                                                               A; Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                        A; Reference number: $70557; MUID:96405918; PMID:8810043 A; Accession: $70559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 54; DB 2
Pred. No. 14;
5; Mismatches
                                                                                           A; Title: Sequence analysis of the CEN12 region
                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: SGD:S0003939; MIPS:YLL016w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1002 PNSNSNNKSQEKSRDDQTDE 1021
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                                                                                                                         e conductance regulator protein CFTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 PNTNKSEKAERKSHDTQTTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.8%;
45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38.8%;
Similarity 45.0%;
9; Conservative
                                       R;Miosga, T.; Zimmermann, F.K.
Yeast 12, 693-708, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: SGD:SCD25; SDC25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: SGD:SCD25; SDC25
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 12L
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Best Local
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Cell 77, 249-259, 1994
A;Title: Mdjlp, a novel chaperone of the DnaJ family, is involved in mitochondrial bioge
A;Reference number: A53500; MUID:94221642; PMID:8168133
A;Accession: A53500
                                                                                                                                                                          A;Cross-references: GB:Z28336; NID:g431909; PIDN:CAA82189.1; PID:g431910
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu
Bubmitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces ce A;Reference number: S56186
                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-511 <MUR>
A;Cross-references: EMBL:D50617; NID:g836685; PIDN:BAA09222.1; PID:g836738; MIPS:YFL016q
R;Murakami, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reywords: heat shock; membrane protein; mitochondrial inner membrane; mitochondrion; 1-55/Domain: transit peptide (mitochondrion) #status predicted <TNP>
56-511/Product: heat shock protein MDJI #status predicted <MAT>
61-125/Domain: dnaJ amino-terminal homology <DNJ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1048 <MIO>
A;Cross-references: EMBL:Z73121; NID:91360186; PID:e245452; PID:91360187; MIPS:YLL016w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NID:91360186; PID:e245452; PID:91360187; MIPS:YLL016w
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A; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals mily and a new ABC transporter homologous to the human multidrug resistance protein. A; Reference number: $69380
A; Accession: $69390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A;Residues: 1-511 <MUW>
A;Cross-references: EMBL:D44596; NID:g1100783; PIDN:BAA08001.1; PID:g1100788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCD25 protein (version 2) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1309; protein YLL016w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Date: 01-Aug-1995 #sequence_revision 24 -May-1996 #text_change 21-Jul-2000
C;Accession: $64758; $64764; $69390; $70559
R;Mosga, T; Zimmermann, F.K.
submitted to the Protein Sequence Database, May 1996
A;Reference number: $647758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology
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*Kooffeau, A.; Purnelle, B.
Submitted to the Protein Sequence Database, May 1996
A; Reference number: $64761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, December 1994 A; Reference number: S62230 A; Accession: S62297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cross-references: SGD:S0001878; MIPS:YFL016c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 PNTNKSEKAERKSHDTQTTQEI 24
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A;Cross-references: EMBL:273121; NII
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 40.3%;
1 Similarity 50.0%;
11; Conservative
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A;Residues: 1-1048 <PUR>
                                                                                                                   A; Molecule type: DNA
A; Residues: 1-511 <RO2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SGD: MDJ1
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A; Residues: 1-737, A', 738-970, I', 972-1250 < DAM2>
A; Residues: 1-737, A', 738-970, I', 972-1250 < DAM2>
A; Notes: references: EMBL:M2664T
A; Note: the authors translated the codon GAG for residue 538 as Asp, GTC for residue
R; Boy-Marcotte, E.; Damak, F.; Camonis, J.; Garreau, H.; Jacquet, M.
Gene 77, 21-30, 1989
A; Title: The C-terminal part of a gene partially homologous to CDC25 gene suppresses
A; Reference number: PSO041; MUID:89306677; PMID:2245538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: CDC25-type guanine nucleotide exchange activator homology F;946-1197/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13
                                                                                                                                                                                                                                                                                                                A; Wolecule type: DNA
A; Residues: 1-1250 < CDAM1>
A; Cross-references: EMBL:M26647
A; Cross-references: EMBL:M26647
B; Damak, F.; Boy-Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M.
Mol. Cell. Biol. 11, 202-212, 1991
A; Title: SDC25, a CDC25-11ke gene, which contains a RAS-activating domain and
A; Reference number: $12942; MUID:91094833; PMID:1986220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as Asp and GAT
                                                                                                             #text_change 06-Feb-1998
SCD25 protein (version 1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1309; protein YLL016w
C;Species: Saccharomyces cerevisiae
C;Dete: 02-Jun-1994 #sequence_revision
C;Accession: S14177; S12942; PS0040
C;Accession: S14177; S12942; PS0040
Submitted to the EMBL Data Library, August 1989
A;Reference number: S14177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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residue 747
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 668-679, 'NPVMTILMC', 689,'N', 691-1250
A; Note: the authors translated the codon GCA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: SGD:S0003939; MIPS:YLL016w
A;Map position: 12L
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 16, 2003, 17:50:14 ; Search time 3.06914 Seconds Run on:

(without alignments) 814.396 Million cell updates/sec

US-09-853-079-195 Perfect score: Title:

139 1 GKPNTNKSEKAERKSHDTQTTQEICE 26 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_73:* Database :

pirl:*
pir2:*
pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

CITACABLEC

		о́Р			SUMMARIES	
Result No.	Score	Query Match	Length	DB	ID	Description
1	60.5	43.5	879	7	T22033	hypothetical prote
7	26	0	511	7	838898	. ધ
m	54	38.8		7	S64758	prote
4	54	8	12	7	S14177	protein
വ	51	36.7		7	F86563	a
9	. 51	36.7	9	7	A72060	
7	20	36.0	196	7	T25445	
æ	20	36.0	4	7	JC5184	G
σ	20	36.0		7	AD2545	hypothetical prote
10	50	36.0		~	D72092	conserved hypothet
11	20	36.0	579	7	C86532	CI082 hypothetical
12	20	36.0		7	G81253	probable oxidoredu
13	20	36.0		7	T37188	presynaptic activi
14	20	36.0		7	869625	hypothetical prote
15	49	2	803	~	T40036	hypothetical prote
16		4	211	-	E69844	GTP pyrophosphokin
17	47		453	7	F71374	probable hemolysin
18	47	B	537		A86444	probable RNA helic
19	47	m	635		F71621	hypothetical prote
20	47	ω.	950		T09076	
21	4		1097		T45622	-
22	46.5	•	65		G81292	_
23	46.5	33.5	1076	7	F96831	
24	46	33.1	57	7	T10457	н
25	46	33.1	N	7	T28053	hypothetical prote
56	46	33.1	283	7	T23785	7
27	46	33.1	æ	7	н90266	Ω
28	46	33.1	. 533	7	S63270	probable membrane
29	46	33.1	608	7	.T25572	hypothetical prote

transcription regu	related to cytochr	protein gp29 - pha	hypothetical prote	hypothetical prote	hypothetical prote	calmodulin - Eugle	salivary qlue prot	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	Balbiani ring 2.1	hypothetical prote	probable lipoprote
B69797	T49758	T13115	T33810	T34243	T19899	MCEG	S01360	T47695	T19313	T46464	T02022	A45294	866719	s62791
2.0	1 (1	7	7	~	7	Н	7	7	7	7	7	7	7	7
761	831	631	881	890	1230	148	263	310	333	542	543	749	761	798
33.1	33.1	32.7	32.7	32.7	32.7	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4	32.4
46	46	45.5	45.5	45.5	45.5	45	45	45	45	45	45	45	45	45
30	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

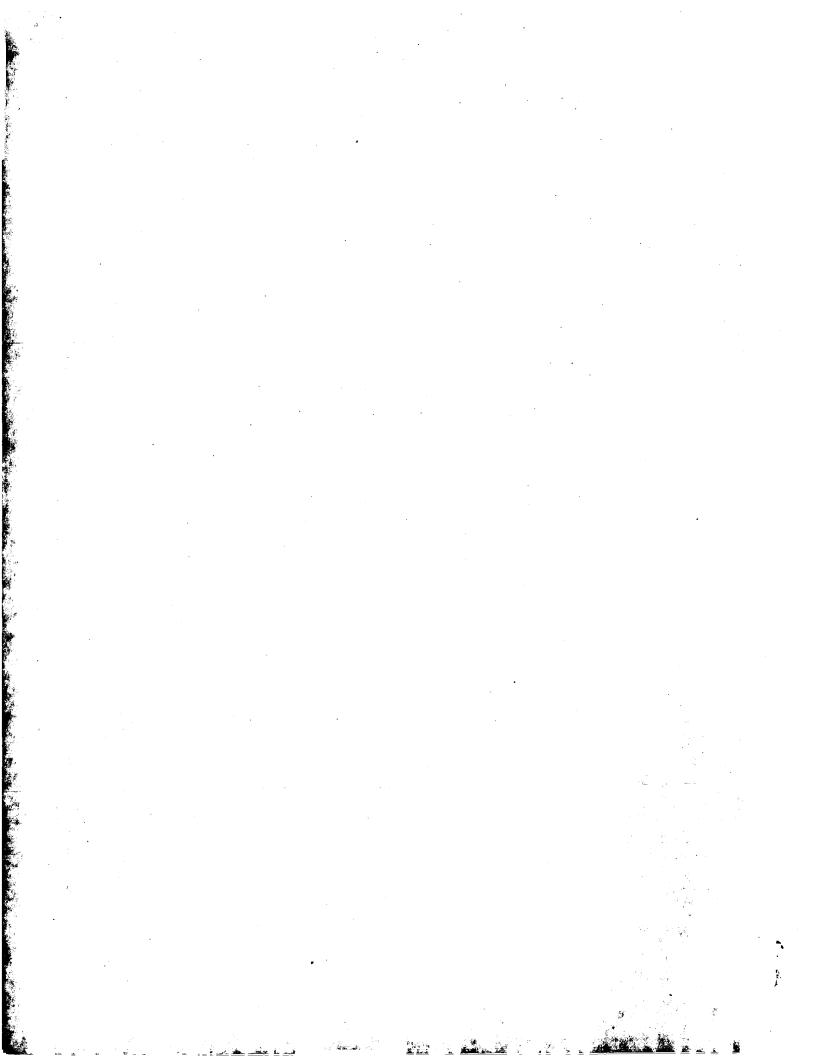
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Cipecies: Caenorhabditis elegans
Cipacies: T2033
R.MacDougall, R.
Submitted to the EMBL Data Library, February 1996
A.Reference number: 219505
A.Recession: T2033
A.Status: preliminary; translated from GB/EMBL/DDBJ
A.Molecule type: DNA
A.Residues: 1-879 -WML>
A.Residues: 1-879 -WML>
A.Cross-references: EMBL: Z69302; PIDN: CAA93261.1; GSPDB:GN00020; CESP: F40F8.5
A.Cross-references: Clone F40F8
C.Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
43.5%; Score 60.5; DB 2; Length 879;
Best Local Similarity 52.2%; Pred. No. 1.4;
Matches 12; Conservative 5; Mismatches 5; Indels 5;
hypothetical protein F40F8.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 2
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A; Introns: 63/1; 149/1; 173/1; 217/1; 262/1; 306/1; 347/1; 381/2; 422/2; 440/3; 461/3

5 TNKSEK-AERKSHDTQTTQEICE 26 3 TNKREKQLERECHEQKTSQAVCE 25 δλ g

RESULT 2

Accession: S48398
heat shock protein MDJ1 precursor - yeast (Saccharomyces cerevisiae)
NA1ternate names: MDJ1 protein; protein YFL016c
C; Species: Saccharomyces cerevisiae
C; Date: 31-Dec-1993 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C; Accession: S38989; A84320; A53500; S56238; S62297
R; RCW-ley, N.K.; Prip-Buus, C; Westernann, B.; Brown, C.M.; Schwarz, E.; Barrell, B.G submitted to the EMBL Data Library, November 1993
A; Description: MdJ1p, a novel DnaJ homologue of Saccharomyces cerevisiae, plays a rol A; McTecnec number: S3898
A; McTecnec number: S3898
A; McTecnec number: BMBL: Z28336; NID: 9431909; PIDN: CAA82189.1; PID: 9431910
B; Churcher, C.
Submitted to the EMBL Data Library, September 1994
A; Reference number: S48320
A; McCession: S48320
A; McCession:



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### APPLICANT: Sleath, Paul R.

### APPLICANT: McNeill, Parricia D.

### APPLICANT: Homer, Mary

### APPLICANT: Homer, Mary

### APPLICANT: Scorist, Heather

### TITLE OF INVENTION: COMPOUNS AND METHODS FOR THE DIAGNOSIS

### TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

### TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

### TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

### CURRENT APPLICATION NUMBER: US/09/737,178

### CURRENT FILING DATE: 2000-12-13

### CURRENT FILING DATE: 2000-12-13

### SOFTWARE: FastSEQ for Windows Version 3.0

### SOFTWARE: FastSEQ for Windows Version 3.0

### SOFTWARE: FastSEQ for Windows Version 3.0

### CONSTRUCTION OF THE OFFICE OFFIC
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US20010029295A1

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 677;
                                                                                                                            APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS FILE REFERENCE: 210121.426C9 CURRENT APPLICATION UNDHABER: US/09/737,178 CURRENT FILING DATE: 2000-12-13 NUMBER OF SEQ ID NOS: 144
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APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
FILLE OF INVENTION: AND TREATMENT OF B. MICROIL INFECTION
FILE REFERENCE: 210121.426C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 139; DB 10; 100.0%; Pred. No. 7.8e-12;
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                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PASLEED for Windows Version 3.0
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Patent No. US20010029295A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 87, Application US/09853079
Publication No. US20030109689A1
GENERAL INFORMATION:
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                                       Houghton, Raymond L.
                                                            APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
APPLICANT: Homer, Mary
Reed, Steven G.
Lodes, Michael J.
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Lodes, Michael J.
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Best Local Similarity
Local 26; Conserva
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Matches 26; Conserv
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ORGANISM: Babesia
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US-09-853-079-87
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                                                                                                                                                                   APPLICANT: Sleath, Paul R.
APPLICANT: MCNelll, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
FILLE OF INVENTION: AND TREATMENT OF B. MICROII INFECTION
FILE REFERENCE: 210121.42669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426211
CORRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
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7.7e-12;
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139;
Best Local Similarity 100.0%; Pred. No. 7
Matches 26; Conservative 0; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 3.0
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 144
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US-09-737-178-144
; Sequence 144, Application US/09737178
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Publication No. US20030109689A1
GENERAL INFORMATION:
                                     Sequence 85, Application US/09737178
Patent No. US20010029295A1
                                                                                                                              Lodes, Michael J.
Houghton, Raymond L.
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Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                    210121.42609
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Best Local Similarity 100.
Matches 26; Conservative
                                                                                                       Reed, Steven G.
Lodes, Michael
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                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TYPE: PRT
; ORGANISM: Babesia
US-09-737-178-85
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US-09-853-079-144
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                  US-09-737-178-85
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APPLICANT:

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TYPE: PRT

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APPLICANT:

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APPLICANT: Boughton, Raymond L.
APPLICANT: Bleath, Paul R.
APPLICANT: Bleath, Paul R.
APPLICANT: Moneil, Patricia D.
APPLICANT: Moneil, Patricia D.
APPLICANT: Becrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS; TITLE OF INVENTION: AND TREPTMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FRASESQ for Windows Version 3.0
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CURRENT APPLICATION NUMBER: US/09/853,079
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
      Indels
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        0; Mismatches
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                                                                 182 GKPNTNKSEKAERKSHDTQTTQEICE 207
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                                              1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                                                          Sequence 211, Application US/09853079
Publication No. US20030109689A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 85, Application US/09853079; Publication No. US20030109689A1; GENERAL INFORMATION:
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sleath, Paul R.
APPLICANT: MCMeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
        26; Conservative
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Best Local Similarity
Matches 26; Conserva
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Best Local Similarity
Matches 26; Conserv
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US-09-853-079-85
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                                                               Length 445;
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APPLICANT: McNeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROII INFECTION
FILE REFERENCE: 210121.42669
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROII INFECTION
                                                                                                          Indels
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                                                             Query Match 100.0%; Score 139; DB 9; Best Local Similarity 100.0%; Pred. No. 4.9e-12; Matches 26; Conservative 0; Mismatches 0;
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Pred. No. 4.9e-12;
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100.0%; Pred. No. 4.5
tive 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001.05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                       182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                                                                                                                1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                                                                                                                                                          Sequence 38, Application US/09853079
Publication No. US20030109689A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McMeill, Patricia D.
APPLICANT: Serrin
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Lodes, Michael J.
Houghton, Raymond L.
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100.0%;
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; ORGANISM: Babesia microti
US-09-286-488-38
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US-09-737-178-38
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Best Local Similarity
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hes 26; Conserv
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US-09-853-079-38
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Sleath, Paul R.
APPLICANT: Movelil, Paul R.
APPLICANT: Movelil, Paul R.
APPLICANT: Movelil, Paul R.
APPLICANT: Movelil, Paul R.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT APPLICATION NUMBER: US/09/737,178
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
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                                                                                                                                                                                                                                                           Length 275;
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michel J.
APPLICANT: Lodes, Michel J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Moneill, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 21012.1.4266
CURRENT APPLICANTON NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                                            Indels
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Pred. No. 2.9e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                           100.0%; Score 139; DB 9; 100.0%; Pred. No. 2.9e-12;
                                                                                                                                                                                                                                                                                                            0; Mismatches
     CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 275
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                           218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 GKPNTNKSEKAERKSHDTQTTQEICE 243
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                                                                                                                                                                                                                                                                                  Best Local Similarity 100.
Matches 26; Conservative
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                                                                                                                                                       TYPE: PRT
; ORGANISM: Babesia microti
US-09-853-079-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Babesia microti
US-09-737-178-53
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Best Local Similarity
Matches 26; Conserva
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APPLICANT: Reed, S
APPLICANT: Lodes, I
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US-09-737-178-53
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LENGTH: 445
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APPLICANT: Sleath, Paul R.

APPLICANT: Momeill, Patricia D.
APPLICANT: Homer, Mary
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS NUMBER: US/09/853,079
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0

LENGTH: 50
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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Patent No. US20020169136A1
Patent No. US20020169136A1
APPLICANT: NEORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOS:
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 139; DB 9;
hilarity 100.0%; Pred. No. 2.9e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 139; D
Best Local Similarity 100.0%; Pred. No. 4.3
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
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APPLICANT: MCNeill, Patricia D.
APPLICANT: Homer, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Babesia microti
US-09-286-488-53
                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: B. microti
US-09-853-079-194
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nes 26; Conserv
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GenCore version 5.1.6 . Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:47:39 ; Search time 4.25295 Seconds (without alignments) 726.026 Million cell updates/sec Run on:

US-09-853-079-195

Perfect score:

1 GKPNTNKSEKAERKSHDTQTTQEICE 26 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

451899 seqs, 118759770 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Published_Applications_AA:*

/cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US10_USDEGONB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBGONB.pep:*/cgn2_6/ptodata/2/pubpaa/US60_PUBGONB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Score	Query Match	Duery Match Length DB	DB	ID	Description
, ;		6	:		
σ	100.0	26	6	US-09-853-079-195	Sequence 195, App
σ	100.0	20	σ	US-09-853-079-194	Sequence 194, App
σ	100.0	275	6	US-09-286-488-53	
σ	100.0	275	σ	US-09-853-079-53	Sequence 53, Appl
σ		275	10	US-09-737-178-53	Sequence 53, Appl
9	100.0	445	6	US-09-286-488-38	Sequence 38, Appl
9		445	6	US-09-853-079-38	Sequence 38, Appl
9		445	10	US-09-737-178-38	Sequence 38, Appl
ð		481	6	US-09-853-079-211	Sequence 211, App
ď		999	6	US-09-853-079-85	Sequence 85, Appl
139		999	10	US-09-737-178-85	Sequence 85, Appl
3		677	6	ت	Sequence 144, App
ď.		677	10		Sequence 144, App
an.	100.0	1132	σ	US-09-853-079-87	Sequence 87, Appl
d)		1132	10		Sequence 87, Appl
'n	82.7	25	σ	_	
œ	56.1	25	σ	US-09-853-079-197	Sequence 197, App
in	46.8	25	6	US-09-853-079-192	192,
m	45.3	32	σ	US-09-286-488-39	Sequence 39, Appl

; Sequence 194, Application US/09853079; Publication No. US20030109689A1; GENERAL INFORMATION:

US-09-853-079-194

RESULT 2

APPLICANT: Reed, Steven G. APPLICANT: Lodes, Michael J. APPLICANT: Houghton, Raymond L.

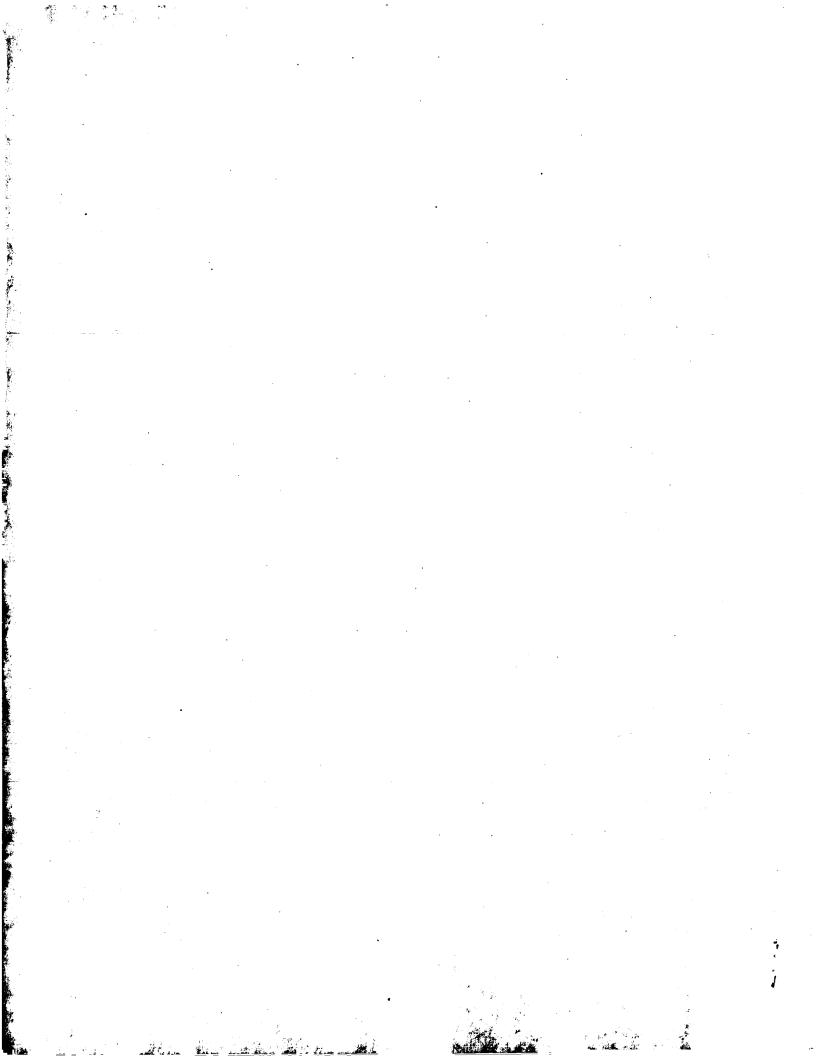
Sequence 39, Appl Sequence 39, Appl Sequence 202, Appl Sequence 202, Appl Sequence 203, Appl Sequence 204, Appl Sequence 542, A	Sequence 542, App
N. C.	9 US-10-175-743-542
32 600 600 255 257 121 178 178 178 178 178 178 178 17	178
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ALIGNMENTS

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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426c11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastESQ for Windows Version 3.0
SEQ ID NO 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 26;
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100.0%; Pred. No. 2.1e-13;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 26; Conservative
                                                                       Publication No. US200301096
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM: B. microti US-09-853-079-195
RESULT 1
US-09-853-079-195
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APPLICANT: MISHRA, LOPA
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT.
FILE REPERBNES: XX/PO470US0
CURRENT APPLICATION NUMBER: US/08/841,349B
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33.8%; Score 47; DB 2; Length 220; 37.5%; Pred. No. 11; tive 5; Mismatches 10; Indels
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Job time: 3.36762 secs
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  ; Sequence 7, Application US/08841349B
; Patent No. 5955594
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 37.5 Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
CORGANISM: Mus musculus
US-08-841-349-7
                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 220
                                                                                                            US-08-841-349-7
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APPLICANT: Margarit, S. M.
APPLICANT: Margarit, S. M.
APPLICANT: Borlock Dafna
APPLICANT: Cole, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
FILE REFERENCE: 600-1-228M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 45.3%; Score 63; DB 4; Length 32; Best Local Similarity 63.6%; Pred. No. 0.0046; Matches 14; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LOCATION: (28)...(28)
OTHER INFORMATION: Xaa - Aspartic Acid or Glutamic Acid
NAME/KEY: VARIANT
INFORMATION: Xaa = Glutamic Acid or Glycine
                                                                                                         LUCATION: (14)...(14)
OTHER INFORMATION: Xaa = Glutamic Acid or Glycine
NAME/KET: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (29)...(29)
OTHER INFORMATION: xaa = Glutamic Acid or Alanine
                                                                                                                                                                    CCATION: (15)...(15)
OTHER INFORMATION: Xaa = Isoleucine or Arginine
NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = Histidine or Tyrosine
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Isoleucine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: VARIANT

LOCATION: (30)...(30)

CHER INFORMATION: Xaa = Cysteine or Histidine
US-09-528-784A-39
                                                                 LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Lysine or Asparagine
                                                                                                                                                                                                                                                                                                                           ION: (23)...(23)
INFORMATION: Xaa = Threonine or Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa = Cysteine or Serine LICARTON: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
BARLIER FILING DATE: 1998-07-21
NUMBER OF SED ID NOS: 14
SOFTWARE: PATENTIN VEY. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 KPNTNKSEKAERKSHDTQTTQE 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: Saccharomyces cerevisiae US-09-356-952-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/09356952 Patent No. 6117663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 38.8°
Best Local Similarity 45.0°
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT
                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1048
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OTHER INFO
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Paul R. COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. MICROTI INFECTION
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or Arg"
                                                                                                                                                                                       ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPATE: PATENTING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
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                                                                                           ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
STRIE: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "Residue can be
                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REGISTROCEPOCKET NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 32 amino acids TYPE: amino acids STRANDEDNESS:
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NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: /note-
OTHER INFORMATION: OF GLY
FEATURE:
NAME/KEY: Modified-site
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LOCATION: 5
O'THER INFORMATION: /note-
O'THER INFORMATION: or lle
FEATURE:
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LOCATION: 3
.OTHER INFORMATION: /note-
OTHER INFORMATION: or Asp
FEATURE:
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                                                        NUMBER OF SEQUENCES: 49
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
APPLICANT: Sleath,
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                            USA
                                                                                                                                                                      COUNTRY:
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodges, Michael J.
APPLICANT: Bloath, Paul R.
APPLICANT: Aleath, Paul R.
APPLICANT: Moneil, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FASTSEQ for Windows Version 3.0
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 32;
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 23
OTHER INFORMATION: /note= "Residue can be either Thr
OTHER INFORMATION: or Pro"
FRATURE:
'NAME/KEY: Modified-site
                                                                                                                                                             /note= "Residue can be either Ile
or Thr"
                                                                                                                                                                                                                                                                                                                                                       /note= "Residue can be either Asp
or Glu"
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or Ala"
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or Ser"
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LOCATION: (3)...(3)
OTHER INFORMATION: Xaa = Glycine or Aspartic Acid
NAME/KEY: VARIANT
LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = Proline or Isoleucine
NAME/KEY: VARIANT
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Pred. No. 0.0046;
0; Mismatches
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OTHER INFORMATION: Xaa = Lysine or Threonine
NAME/KEY: VARIANT
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                                                                                                  MAMME/KEY: Modified-site LOCATION: 26 OTHER INFORMATION: Or Thr. FATURE:
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LOCATION: 27
OCHER INFORMATION: /note
OTHER INFORMATION: or SE
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COCATION: 30

LOCATION: 70

OTHER INFORMATION: Or Hi

US-08-723-142A-39
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Best Local Similarity 63.6'
Matches 14; Conservative
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ORGANISM: Babesia microti
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OTHER INFORMATION:
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NAME/KEY: Modified-
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LOCATION: 15
LOCATION: 15
O'THER INFORMATION: /note= "Residue can be either Ile
O'THER INFORMATION: or Arg"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
O'THER INFORMATION: /note= "Residue can be either His
O'THER INFORMATION: or Tyr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 23
LOCATION: 23
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                                 /note= "Residue can be either Glu or Gly"
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or Glu"
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or Ala"
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
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                                                                                                             LOCATION: 12
OTHER INFORMATION: OTHER INFORMATION: OT ASN'
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NAME/KEY: Modified-site
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LOCATION: 27
OTHER INFORMATION: /
OTHER INFORMATION: 0
FEATURE: MODIFIED-s
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LOCATION: 29
OTHER INFORMATION:
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FEATURE:
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COTHER INFORMATION:
US-08-990-571-39
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OTHER INFORMATION:
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LOCATION:
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   NAME/KEY:
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APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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Pred. No. 0.0046;
0; Mismatches 8; Indels
                                       /note= "Residue can be either Glu
or Ala"
                                                                                                                                /note= "Residue can be either Cys or His"
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or Thr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                        4 KXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                   2 KPNTNKSEKAERKSHDTQTTQE 23
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/08990571 Patent No. 6214971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                          Query Match
Best Local Similarity 63.6%;
Matches 14; Conservative
                                                                                           NAME/KEY: Modified-site LOCATION: 30
 Modified-site
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NAME/KEY: Modified-
LOCATION: 29
OTHER INFORMATION:
OTHER INFORMATION:
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COTHER INFORMATION:
US-08-845-258-39
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CITY: Seattle
STATE: Washington
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OTHER INFORMATION:
FEATURE:
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US-08-990-571-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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                                                                            FEATURE:
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us-09-853-079-195.rai

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LOCATION: 28
OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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FEATURE:
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NAME/KEY:
LOCATION:
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NAME/KEY:
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NAME/KEY:
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                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                     JOHERANI INCOMENTATION OF TEACH OF APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Bleath, Paul R.
APPLICANT: Bleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION FILE REFERENCE: 20121.42664
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; DB 4; Length 1132;
8.3e-13;
nes 0; Indels 0
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Aleath, Raymond
APPLICANT: Sleath, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEA AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                              Query Match 100.0%; Score 139; DB 4; Length 666; Best Local Similarity 100.0%; Pred. No. 4.5e-13; Matches 26; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 100.0%; Score 139; I
Best Local Similarity 100.0%; Pred. No. 8.3
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                          1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                                                                                                                                                                  Sequence 87, Application US/09528784A Patent No. 6451315
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STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Babesia
US-09-528-784A-87
; ORGANISM: Babesia
US-09-528-784A-85
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/note= "Residue can be either Gly or Asp"
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or Asn"
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or Thr"
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or Glu"
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or Arg"
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or Pro"
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REGISTRATION VUNBER: 21,392
REGISTRATION VUNBER: 210121.426C1
TELECOMNUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /note-
OTHER INFORMATION: or Asn'
FEATURE:
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NAME/KEY: Modified-site
LOCATION: 5
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14
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23
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28
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                                                                                                                                          LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
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LOCATION: 18
OTHER INFORMATION:
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Fatent No. 6451315

GENERAL INFORMATION:
APPLICANT: Redes, Steven G.
APPLICANT: Bodes, Michael J.
APPLICANT: Glath, Paul R.
APPLICANT: Glath, Paul R.
APPLICANT: Glath, Paul R.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFRENCE: 210121.42664
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                            Length 445;
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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REPERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 GKPNTNKSEKAERKSHDTQTTQEICE 207
      REFERENCE/DOCKET NUMBER: 210121.426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                 TELECOMMUNICATION INFORMATION TELEPHONE: (206) 622-4900
                                                                                         TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 26; Conservative
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Matches 26; Conservative
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US-09-528-784A-38
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APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                ; TOPOLOGY:
US-08-723-142A-38
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
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Patent No. 6306396
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Bleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION COMPOUNDS AND ADDRESS AND A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 445;
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                                                                                                                                                                                                                                           ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/990,571
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                         ADDRESSEE: SEED AND BERRY STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
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100.0%; Pred. No. 2.8
Live 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
REFERENCAMUNICATION INFORMATION:
TELECHOMNE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MBER: US/08/990,571
11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0
Matches 26; Conservative
                                 NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                           CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TOPOLOGY: linear
US-08-990-571-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Steven G.
APPLICANT: Rodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIACNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 445;
                                                                                                                          Length 275;
                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6300 Columbia Center, 701 Fifth Avenue
                                                                                                                        Score 139; DB 4;
Pred. No. 1.6e-13;
                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                 1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 Sequence 38, Application US/08845258 Patent No. 6183976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G. et al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-990-571-38
; Sequence 38, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/ACENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                        Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 26; Conservative 0;
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Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (206)682-6031
                                        TYPE: PRT
ORGANISM: Babesia microti
US-09-528-784A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
  SEQ ID NO 53
LENGTH: 275
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                                                                                                                                         Sequence 53, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 275;
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APPLICANT: Sleath, Paul R.
APPLICANT: MCNE111, Pauticia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121,426C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                        6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 139; DB 4;
Best Local Similarity 100.0%; Pred. No. 1.6e-13;
Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 210121.426C2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/528,784A CURRENT FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
                       218 GKPNTNKSEKAERKSHDTOTTOEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEPRA: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                         SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia Microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 275 amino acids
amino acid
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
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                                                                                                                                                                                                                                                                                           ADDRESSEE:
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                                                                                                                      US-08-990-571-53
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 16, 2003, 17:42:54; Search time 2.36762 Seconds Run on:

(without alignments) 323.107 Million cell updates/sec

US-09-853-079-195

Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

262574 seqs, 29422922 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:* Issued_Patents_AA:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		on	53, Appl	53,	53,	38, Appl	٠,,	38,	38,	85,	87,	39,	39,	39,	39,	5, A	,	4, Appli	6	13,	565	10, Appl	10,	10,	10,	17,	19,	8,	36
		Description	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
SUMMARIES	4	ID	US-08-845-258-53	US-08-990-571-53	US-09-528-784A-53	US-08-845-258-38	US-08-990-571-38	US-08-723-142A-38	US-09-528-784A-38	US-09-528-784A-85	US-09-528-784A-87	US-08-845-258-39	US-08-990-571-39	US-08-723-142A-39	US-09-528-784A-39	US-09-356-952-5	US-08-841-349-7	US-08-841-349-4	US-09-185-160-9	US-09-185-160-13	US-09-134-001C-5651	US-08-348-792-10	US-08-462-738-10	US-09-199-955-10	US-08-880-875-10	US-08-131-625B-17	PCT-US95-10904-19	US-08-691-814B-8	US-09-134-001C-3955
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	1	Length	275	275	275	445	445	445	445	999	1132	32	32	32	32	1048	220	2154	259	734	219	343	343	343	343	123	123	534	576
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		Score	139	139	139	139	139	139	139	139	139	63	63	.63	63	54	47	47	46	46	45.5	44	44	44	44	• 43	43	43	43
	Result	NO.	1	7	Э	4	2	9	7	8	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27

351 11,	508	Sequence 37, Appl Sequence 26, Appl	Sequence 4, Appli Sequence 26, Appl	27,	Sequence 2, Appli	12,	Sequence 12, Appl	Sequence 12, Appl	Sequence 23, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 13, Appl
US-09-134-001C-3517 US-09-185-160-11	US-U8-244-189-2 US-09-134-001C-5080	US-U8-469-26UA-3/ US-08-463-587A-26	US-08-463-667A-4 US-08-923-854-26	PCT-US91-09133-27	US-09-352-990-2	US-08-889-419-12	US-08-402-542-12	PCT-US93-07189-12	US-08-687-956A-23	US-08-296-791-6	PCT-US95-10661A-6	US-08-799-464A-13
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200	31	33	34 35	36	37	3 6	40	41	42	43	44	45

ALIGNMENTS

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Gaps
                                                               GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Bloath, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Scattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCH COMPATIBLE
COMPUTER: DATENTINE RELEASE #1.0, Version #1.30
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210121.426C1
                  Sequence 53, Application US/08845258 Patent No. 6183976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia Microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM:
US-08-845-258-53
US-08-845-258-53
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VMKE 438	SEGN 185 : HH 493	RDDG 237 RPS- 542	A 282 GEIS 596	-TCA 318 	SNGT 377 	414 JLNKH 772	420 WRPKQ 832	rGA-G 470 	
VPDEILSQKSPKFAIRHTATGIISHVDSAAVSALGYLPQDLIGRSIMDFYHHEDLSVMKE	IXHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN	NMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG 	YDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKA :	:FDECKSNAIILKKKILDNDEDYKINFREMVNEVTCA : : :	NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAV-TVSVSATSNGT :	ESG-GAGSGTGTSV-SATSTLTGNG-GTESGGTAGTTTSS) NDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGGSHSWEGEANKPKQ	-TSGTTTSSGAASGKAG-TGTAGTTTSSEG-AGSDKAGTGTSGTTTSSGTGA-G	GAGSGGPSGHASNA 484 : : GAGGGGAGAAAA 906
379	129	186	238	283	319	378	415	421 _.	471
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Search completed: July 16, 2003, 17:50:04 Job time: 125.145 secs

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Length 1218;
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SMART; SMO0091; PAS; 2.
PROSITE: PSO0225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
SEQUENCE 1218 AA: 127363 MW; 8506C15999F78AE3 CRC64;
              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5;
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InterPro; IPR0010610; PAC.
InterPro; IPR000014; PAS_domain.
Pfam; PP00989; PAS; 2.
01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                       PER protein.
PER OR EG:155E2.4 OR CG2647.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22.68;
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Matches 139; Conserv
                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                         356 TYIVGAGVEAVTVSVSATS-NGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTEAGGTSGT----TISSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---NREE 282
                                                                                                           340 LTTEIDNNIEQISSY-----KSEITELRRNVQALE-----IELQSQLALKQSLEASL 386
                                                                                                                                                                                                 343 DVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGT 402
                                                                                                                                                                                                                           NEIQTYRSLLE-----GEG------GGG------GGG 465
                                                                                                                                                                                                                                                       ESGGTAGTTTSSGTEAGGTS----GTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGT 458
                                                                                                                                                                                                                                                                      466 YGGGSSGGSSGGTGGSSSGGHGGSSSGGYGGGSFGGGGGGGGGGSSGG-GY 524
                          173 FIEKLRGARSEGNNMFQEA-----LIRFRNASSEEMVNAASYLSAALFRYKEFDDE
                                                   283 EMKHLRNVSTGDVNVEMNAAPGVDLTQLLNNMRN-QYEQLAEQNRKDAEAWFNEK--SKE
                                                                                  LFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAF
                                                                                                                                         DECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKIN-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xiao L., Li L., Visvesvara G.S., Moura H., Didier E.S., Lal A.A.; "Genotyping Encephalitozoon cuniculi by Multilocus Analyses of Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
LRQSVEADI ----NGLRRVLDELTLTQADLEMQIESLTEELAYLKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                         01-DEC-2001 (TTEMBLE-1.1), Last sequence update)
01-JUN-2002 (TTEMBLE-1.21, Last sequence update)
Spore wall protein-1 (Fragment).
Encephalitozoon cuniculi.
Eukaryota, Macrosporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 AA; 9983 MW; 30AE862B0D66643E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.7%; Score 197; DB 5; 35.3%; Pred. No. 0.0098;
                                                                                                                                                                                                                                                                                                                                                                                                                125 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1218 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34; Mismatches
                                                                                                                                                                                                                                                                                                                              525 GGGSSGGGYGGSSSGGHKSSSSGS 550
                                                                                                                                                                                                                                                                                                              SGTTTSSGTGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         with Repetitive Sequences.";
J. Clin. Microbiol. 39:2248-2253(2001).
EMBL; AF340011; AAK63051.1; -.
PRINTS; PR01574; TUBBTPROFEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=USP A-2;
MEDLINE=21270266; PubMed=11376065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGSGGPSGHASN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |:|||| || :|:
| GSGSGGESGGSSS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                 224
                                                                                                                                         284
                                                                                                                                                                                                                          437
                                                                                                                                                                                                                                                                                                            4 <u>5</u> 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 15
Q9W4X0
ID Q9W4X0
AC Q9W4X0;
                                                                                                                                                                                                                                                                                                                                                                                                             Q964C1
                                                                                                                                                                                                                                                                                                                                                                                 RESULT 14
0964C1
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REDILING-20196606; PubMed=10731132;

RA Admas M.D. Celnikers S.E., Holt R.A., Googyne J.D.,

RA Admas M.D. Celnikers S.E., Holt R.A., Googyne J.D.,

RA Admas M.D. Celnikers S.E., Li P.M., Hookins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.H.C., Blazef R.G., Champe M., Pfelifer B.D.,

RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Apbayani A., Baxendale J., Bayaktaroglu L., Beasley E.M.,

RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,

RA Bellew R.M., Basu A., Baxendale J., Brokaten P., Borttier P.,

RA Benson K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dalike C., Davenport L.B., Davises P.,

RA Cherry J.M., Cawley S., Dalike C., Davenport L.B., Davises P.,

RA Cherry J.M., Cawley S., Dalike C., Davenport L.B., Davises P.,

RA Cherry J.M., Cawley S., Dalike C., Davenport L.B., Davises R.,

RA Cherry J.M., Cawley S., Dalike C., Davenport L.B., Davises R.,

RA Cherry J.M., Cawley S., Dalike C., Bavenport L.B., Davises R.,

RA Cherry J.M., Cawley S., Dalike C., Rerraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferraz C., Ferras C., Gabriellan A.E., Gagn N.S., Dunkov B.C., Dunkov B.C.,

RA Glodek A., Goog F., Gorrell J.H., Gu Z., Genbart W.M., Calasser K.,

RA Haris N.L., Harvey D., Henhand T.J., Hernandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Alazis M., Murphy B. W., Murphy B., Murphy L., Muzay D.M., Noshrefi A.,

Rako P., Lei Y., Levitsky A.A., Li J., Li Z., Linny Y.,

Rako P., Lei Y., Levitsky A.A., Li J., Li Z., Linny Y.,

Rako P., Lei Y., Walson K.A., Nixon K., Nusskern D.R., Sulth T.,

Ray Shier E., Spradiling A.C., Sauders R.D., Scheeler F., Shen H.,

Ray Shier E., Spradiling A.C., Sauders R.D., Scheeler F., Shen H.,

Ray Shier E., Spradiling A.C., Sauders R.D., Scheeler F., Shen Y.,

Ray Shen R.F., Zaveri J.S., Zhon N., Vanny R., Shung X.,

Ray Shen R.F., Zaveri J.S 79 TPADV-AGVSDGFFIRGONLGAVGSVNE------QPNTVGMSLEQFIKNELYSFSNE 128 25 GEVTSNFRYISKEYEYEHTEL-----AKEHCKKEKCVNVDNIEDNNLKIYAKQFKSVVT 78 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

us-09-853-079-52.rspt

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Pfam; PF00038; filament;
                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Human)
                                                                                                           1079 AA;
                                                                                 Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coiled coil;
                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Keratin 10
                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131
                                                                                                                                                                                                                                                                                              465
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                                                                                                                                    Query Match
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                                                                                                                                                    Best Local
                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                  ----KAGTGTAGTTTSSE 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAGSDKAG----TGTSGTTTSSGTG-----AGGA------GSGGP 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 493 GGGSAAAGGVSESSSGGSTAAGGTSESASGGSATAGGASGGTYTDSTGGSPTGSPSAGGP 552
                                                                                                                                                                                                                                       "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>`</u>
                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PGRS-family protein (Fragment).
RV3512 OR MYV023.19
RV3512 OR MYV023.19
RV3512 OR ALIMETINE TREATMENT.
Bacteria Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Coldon S.V., Eiglmeder K., Gas S., Barry C.E., III, Tekaia F., Badcook K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Stuter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                                  s.;
                                                                                                                                                                                                                                                                                                                                                                           63;
                                                                                                                                                                                                                                                                                                                                              7.7%; Score 198.5; DB 10; Length 614; 33.5%; Pred. No. 0.048;
                                                                                                                                             Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   360 GAGVEAVTVSVSATSNGT-ESGGAGSGTGTSVSA-TSTLTGNGGTESGG-
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                    614 AA; 54412 MW; C522ADFC4062F06B CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 3, BAC clone: T19N8.
Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                          40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 1079 AA.
                                                                                                                                                                                                                                                                                                                                                                          24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---TAGTTTSSGTEAGGTSGT-TTSSGAASG-
                                                                                                                                                                                                STRAIN-COLUMBIA;
MEDLINE-20363099; PubMed-10907853;
                                                                                                                                                                                                                                                             TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP002057; BAB03175.1; -.
HSSP; P41140; 2SFA.
                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGHASNAKIPG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSASESSMEG 563
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                STRAIN-COLUMBIA;
                                                                                          NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1773;
                                                                                                                                                                                                                        Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-H37RV
                                                                                                                                                                                                                                                                                                                                                                        64;
                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          448
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                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                             Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   053557;
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                                                                                                                                                                                                                                                                                                                                                                          Matches
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 QQ
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360 GAGVEAVIVSVSATSNGTESGGAGSGTGTSVSATSTLT----GNGGTESGGTAGTITSSG 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 T - - GGDGALAGSSGGAGGKGGNGGDAGKAGTGSAPGTAGTGGDGGKGGNGGIGAAGTTGP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGGLLSGNEKVTMQNLNDRLASYLDKVRALEESNYELEGKIKERYDQHGNSRQGEPRDYS 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 KQFKS-----VVTTPADVAGV-----SDGFFIRGONLGAVGSVNEQPNTVGMS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           191 KYYKTIDDLKNQILNLTTDNANILLQIDNARLAADDFRLKYEN------EVA 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         416 TEAGGTSGTTTSSGAA-----SGKAGTGTA-GTT-TSSEGAGSDKAGTGTSGTTTS 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GNGADNTTTAAAGTTGGAGGAGGAGGTGGTGGAAGTGTGGQQGNGG--NGGNGGTGGKGG 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DGSLLASGEVTS----NFR---YISKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
TISSUE-FORESKIN BPIDERMIS;
Zhou X.M., Idler W.W., Steven A.C., Roop D.R., Steinert P.M.;
Zhou X.M., Idler W.W., Steven A.C., Roop D.R., Steinert P.M.;
"The complete sequence of the human intermediate filament chain keratin 10. Subdomainal divisions and model for folding of end domain sequences.";
                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 125;
                                                                                                                                                                                                                                                                                                               Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 263:15584-15589(1988).
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
EMBL; JOHOUS9; ARAGOS44.1; -.
InterPro; IPRO01564; IF.
InterPro; IPRO01564; IF.
                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                   81163 MW; A79718CDCB74B97D CRC64;
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561 AA; 57247 MW; D647489FF26E157C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7%; Score 197.5; DB 4; Best Local Similarity 21.7%; Pred. No. 0.049; Matches 110; Conservative 74; Mismatches 197;
                                                                                                                                                                                                                                                                                                                                                                      57;
                                                                                                                                                         PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                         DB 16;
                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 0.095; 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGTGA-----GGAGSGGPSGHASNAKIPG 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 VGTGASGGTGGSGGAGGTGGDGGAANGGTAG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 AA.
                                                                                                                                                                                                                                                                                                               Score 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
complete genome sequence.";
Nature 393:537-544(1998).
BMBL; AL022022; CAA17749.1; -.
TUDErCULIST; RV3512; -.
InterPro; IPR002202; HMG-COA_red.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR01248; TYPE1KERATIN. PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                            7.78;
37.78;
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01,
19,
                                                                                                                                                                                                                                                                                                                                         Similarity 37.7
57; Conservative
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TISSUE-MANTLE;

MEDLINE-98070424; PubMed-9405458;

MEDLINE-98070424; PubMed-9405458;

ABDLINE-98070424; PubMed-9405458;

ABDLINE-98070424; PubMed-9405458;

ABDLINE-98070426; But and a matrix protein of trom shell and pearl nacre of Haliotis rufescens.";

J. Balol. Chem. 273.2472-23481(1997).

THE SHELL. MAY ALSO PERFORM OTHER FUNCTIONS SUCH AS INTERACTING WITH POLYANIONIC ARGONITE-DETERMINING PROTEINS, PROTEING THE PROTEIN COMPONENTS OF THE MATRIX PROM DEGRADATION, AND CONFERRING ELASTIC RESILIENCE TO THE MICROLAMINATE COMPOSITE OF THE SHELL.

SUBCELLULAR LOCATION: EXTRACELLULAR, SYNTHESIZED AND SECRETED SPECIFICALLY BY THE MANTLE PALLIAL CELLS.

SPECIFICALLY BY THE MANTLE PALLIAL CELLS.

ODMAIN: THE PROTEIN CONTAINS TEN HIGHLY CONSERVED CYSTEINE-RICH DOMAINS

COMMAIN: THE PROTEIN CONTAINS TEN HIGHLY CONSERVED CYSTEINE-RICH DOMAINS

NEAREST THE C TERMINUS, AND THESE ARE FOLLOWED BY A BASIC DOMAIN

NEAREST THE C TERMINUS, AND THESE ARE FOLLOWED BY A BASIC DOMAIN
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                         Haliotis rufescens (California red abalone).
Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
Haliotidae; Haliotis.
NCBI_TaxID=6454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYS-RICH.
ARG/LYS-RICH (BASIC).
TO LORICRIN.
N-LINKED (GLCNAC. . .) (E
N-LINKED (GLCNAC. . .) (E
N-LINKED (GLCNAC. . .) (E
                                                                                                                 044341 PRELIMINARY; PRT; 1428 AA.
044341;
01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF022459; AAB95154.1; -.
HSSP; P19957; ZREL.
InterPro: IPR002221; WAP.
InterPro: IPR002899; WRL/EB.
PRINTS; PR00003; 4DISULPHCORE.
SWART; SW00239; WRL; 4.
PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_2.
Structural protein; Glycoprotein.
                          445 SSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGG 476
                                     586 GGSGGGGSSGGSYGG---SSGGGRGGSSSGG 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYS-RICH.
GLY/SER-RICH.
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CYS-RICH.
PRO-RICH.
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PRO-RICH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein.
108 CYS-
                                                                                                                                                                                                                                                         [1]
SEQUENCE FROM N.A.
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                                                                                                                                                                                        LUSTRIN A.
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EALNDLIISDCEKKGIKINRDVISSYKLLLSTI-TYIVGAGVEAVTVSVSATSNGTESGG 381
                    AGSGTGTSVSATSTLTGNGGTESGGT----AGTTTSSGTEAGGTSGT----TTSSGAASGK 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P1,
                                                                                                                                                                                         01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 3, BAC clone: T19N8
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae: Streptophyta: Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
       SAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKK-ELVI--LASVLDGLDLIMERLI
                                                  ENFSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEV--TCANTKFEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                   "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP002057; BAB03182.1; -.
SEQUENCE 342 AA; 31165 MW; B78F9602BCD914A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTGTAGTTTSSEG--AGSDKAGTGT-SGTTTSSGTG-AGGAGSGGPSGHAS 482
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                                                                                                                                                                                                                                                                                                                             Tabata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0 day neonate head cDNA, RIKEN full-length enriched library, clone:4833436C19, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                         Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Te
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.1%; Score 209; DB 10;
10.1%; Pred. No. 0.0081;
.ve 24; Mismatches 57;
                                                                                                                  506
                                                                                             326 NDLIISDCEKKGIKINRDVISSYKLLLSTITY 357
                                                                                                                                                                        342 AA
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                                                                                                              EDITITATC----KHNNPVLIRFSCSIEKYYY
                                                                                                                                                                       PRT;
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MEDLINE-20363099; PubMed=10907853;
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Best Local Similarity 40.1%
Matches 69; Conservative
                                                                                                                                                                       PRELIMINARY;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                           Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323
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Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Rajazawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Rakell P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,
Rakell P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,
Rakel P., Nokido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Rakel K., Okido T., Furuno M., Carninci P., de Bonaldo M.F.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Radustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Iyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Rotrone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whyshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Wangachizaki V., Vanga K., Rawaji H., Kohtsuki S.,
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245 ILRRKVDSLKSDQSRMDSELKNMQDLVEEYRTKYYEDEINKRTNAENEFVIIKKDVDSAYM 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---- DVNNTDDIKKAFD 284
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Eutheria; Rodentia; Sciurognathi; Muridae; Mus Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               330 ----ISDCEKKGIKINRDV---
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                                                                                                                                                      STRAIN-C57BL/6J; TISSUE-HEAD;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR001664; IF.
Interpro; IPR0002957; Keratin_I.
Interpro; IPR003054; Keratin_II.
Interpro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00038; filament; 1.
PRINTS; PR00341; PRION.
PRINTS; PR01278; TYPE1KERATIN.
PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; UNRNOWN.1.
SEQUENCE 637 AA; 65627 MW; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 409:685-690(2001).
EMBL; AK019521; BAB31776.1; -.
MGD; MGI:96698; Krt2-1.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
9
                                                                                                                                                                                                                                                                                                                                             Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
A Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toritumi M., Yu G.
A Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toritumi M., Yu G.
A Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
Jones T., Kamiya A., Karlin-Neumann G., Kawal J., Kim C., Koesema E.,
A Jones T., Kamiya A., Karlin-Neumann G., Kawal J., Kim C., Koesema E.,
A Jones T., Kawiya A., Karlin-Neumann G., Kawal J., Kim C., Koesema E.,
A Jones T., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
A Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
A Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
T Full Length coll to the EMBL/GenBank/DbBJ databases.
B Submitted (MAY-2001) to the EMBL/GenBank/DbBJ databases.
B EMBL, AC001645; AAB63631.1; ...
B EMBL, AV035108; AAK59613.1; ...
B RSP; P18670; LJAC.
B IRFEPPO; IPR001229; Jacalin_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418 AGGISGITISSGAASGKAGTGIAGITISSEGAGSDKAGTGISGITISSGTGAGGAGSGGP 477
                                                                                                                                                                                                                                                                             "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                        STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Ketchum K.A., Phillips C.A., Brandon R.C.,
Fuhrmann J.L., White O., Kerlavage A.R., Adams M.D., Somerville C.R.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GAGVEAVTVSVSATSNGTESG-GAGSGTGTSVSATSTLTGNGGTESG-GTAGTTTSSGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus (Rape).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.
NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.1%; Score 234.5; DB 10; Length 705; 46.1%; Pred. No. 0.0011;
                                                                                                                                                               STRAIN-COLUMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42; Indels
                                                                                                                       Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72473 MW; DC7F51FC0FD39C05 CRC64;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAX-2002 (TrEMBLrel. 20, Last annotation update)
Jasmonate inducible protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  680 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                       DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01419; Jacalin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SGHASNAK 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            246 TGTGSGAO 253
                                                                                                                                                                                                                                                                                                           and BAC clones.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                SEQUENCE FROM N.A.
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                        FROM N.A.
                                                                                                                                                                                                                                                   PubMed=10907853;
                                                                                                                                                                                                                                                                   Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478
                                                                                                                                                                                                                        SEQUENCE
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P93658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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       AC DT DT DT OC OC OC OC OC OC OC
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                                                                                                                                                                                                                                                                                                                                                                                                  373 TSNGTESGGAGSGT-GTSVSATST-LIGNGGTESGGT-AGTTTSSGTEAGGTSGTTTSSG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                    430 AASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGT-----GAGGAGSGGPSGHAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 DNIEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM--SLEQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           155 YILKKEGEGCEQIYNYEEFIEKLRGARSEGNNMFQEALIRFRNASSEEMVN----AASYL 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :| : |: |: |: |: 312 PVLIRFSCSIEKYYY--YFYSMNNTNKWNNHNLKYDNRFKEHSDKNGINYYEISAFKW 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --KHDN 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEYEHTELAKEHCKKEKCVN--V 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D., Benson D.R., Krause P.J., Reed S.G., Persing D.H.; "Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBL_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
Geshi N., Brandt A.;
"Two jasmonate inducible proteins from Brassica napus seedlings homoLogous to myrosinase binding proteins and jacalin.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
EMBL; Y11483; CAA72271.1;
HSSP: P18670; 1JAC.
                                                                                                                                                                                                                                                                                                                                           12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                    Query Match 8.4%; Score 216; DB 10; Length 680; Best Local Similarity 44.4%; Pred. No. 0.008; Matches 55; Conservative 8; Mismatches 49; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Mismatches 149; Indels
                                                                                                                                                                                                 Pfam; PF01419; Jacaiin; 4. SEQUENCE 680 AA; 69937 MW; 8CDOCF16C30CA1E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
17AF410231C431DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Seroreactive antigen BMNI-8 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 FIKNELYSFSNEIYHTISSQISNSFLIMMSDAIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0.011;
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23.5%; Pred. No. 0
                                                                                                                                                                       InterPro; IPR001229; Jacalin_lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babosia microti.";
Infect. Immun. 68:2783-2790(2000).
EMBL; AF206251; AAF68244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20231818; PubMed-10768973;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             592 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          483 NAKI 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              249 VAKI 252
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PSEAGWSSERF-GYQLLPYSRRI--VIFNEVCLSYIYKHSVMILERDRVNDGHKDYIEEK 155
DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 372
                                       LSAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLI
                          DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNTVGMSLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVK-----HDNYI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 TKEKNKLKKELEKC-----FPEQY-----SLMKKEELARIFDNAST-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----LKKEGEGCEQIYNYEFIEKLRGARSEGNNMFQEALIR-FRNASSEEMVNAASY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
                                                                               AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG
                                                                                             Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia
                                                                                                                                                                                                                                                                                                                                                      Mohamath R., Reynolds L.D.
                                                                                                                                                                                                                                                                                                                                      MEDLINE=20231818; PubMed=10768973;
Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L
Benson D.R., Krause P.J., Reed S.G., Persing D.H.;
"Serological expression cloning of novel immunoreactive antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLEL). 04, Last sequence update)
01-MAR-2002 (TrEMBLEL). 20, Last annotation update)
Jasmonate inducible protein ISOLOG (Jasmonate inducible protein,
myrosinase binding protein-like) (Putative jasmonate inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISDCEKKGIKINRDVISSYKLLLSTITYI -----VGAGVEAVTVSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                        Infect. Immun. 68:2783-2790(2000).
EMBL, AF206245, AAF68236.1; -.
SEQUENCE 362 AA; 39988 MW; 1B88DCFEF2BD5133 CRC64;
                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.3%; Score 239.5; DB 5;
29.3%; Pred. No. 0.00031;
11ve 50; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    705
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                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                             Seroreactive antigen BMN1-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                                                               Babesia microti
                                                                                                                                                                                                                                                          Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Sim-
85;
                                                                                                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                              STRAIN-MN1
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T02004.4.
                                                                               361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210
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                          301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  004310;
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                                                                                                                                                                            Q9NIP1
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09NIP1
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 ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                        DEDYKINFREMVNEVTCANTKFEALNDL11SDCEKKGIK1NRDV1SSYKLLLST1TY1VG
                                                                                                                                                 AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG
                                                                                                                                                                                                     1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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                                                                               DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN
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                            RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
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NCBI_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 492;
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Last annotation update)
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Babesia microti.
                                                                                                                                                                                                                                                                                                              Created)
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EMBL; AF206246; AAF68238.1; -.
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nes 417; Conservative
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08y293 ralstonia s O9uve7 yarrowia li 08teg1 saccharomyc 0964c5 encephalito 05.5559 mycobacteri 08viy9 mycobacteri 008294 saccharomyc

Q964c2 encephalito Q9ninO babesia mic

091999 cynomolgus 053552 mycobacteri 08421 mycobacteri 048031 haemophilus 0900c2 plasmodium 0944m4 drosophila 01840 canis famil 084020 myxococcus 085783 myxococcus 065783 mycobacteri 053775 mycobacteri 053775 mycobacteri 091841 mycopasma

Scoring table:

Searched:

Database

Perfect score:

Sednence:

OM protein

Run on:

Q901m9 babesia mic Q8vk71 mycobacteri Q8vj15 mycobacteri Q8vj20 mycobacteri Q8vizO uycobacteri Q9zb39 ureaplasma

O9pf60 xylella fas

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1 RRENEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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NCBL_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D. Benson D.R., Krause P.J., Reed S.G., Persing D.H.; "Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 2565; DB 5; Length 503; 100.0%; Pred. No. 5.2e-114; Live 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1
503 AA; 53831 MW; 0098D5DBF1BBF5AA CRC64;
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Last annotation update)
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                  0964C2
09NIN0
09NIN0
08YZ93
0964C5
053559
08YZ94
091P09
053552
083552
099U0C2
099U0C2
099U0C3
099U0C3
099U0C3
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099U0C3
099U0C3
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Q969D4
Q9NIM9
Q8VK71
Q8VJ15
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MEDLINE=20231818; PubMed=10768973;
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Infect. Immun. 68:2783-2790(2000).
EMBL; AF206247; AAF68239.1; -.
HSSP; P00778; 1GBJ.
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SEQUENCE FROM N.A.
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09NIN8
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Q9nin9 babesia mic
Q9nip1 babesia mic
004310 arabidopsis
P93658 brassica na
Q9nin3 babesia mic
Q91h90 arabidopsis
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Q964c4 encephalito
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848.513 Million cell updates/sec
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                                                                                                                                                                                                                                                              1 KRFNEHTDMNGIHYYYIDGS......AKIPGIMTLTLFALLTFIVN 503
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                                                                                                                                      July 16, 2003, 17:37:48 ; Search time 122.145 Seconds
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                              671580 seqs, 206047115 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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004310
P93658
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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sp_archeap:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 2000000000
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Match Length DB
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091197 arabidopsis 053557 mycobacteri 014664 homo sapien 0964c1 encephalito 0994XO drosophila 061869 mus musculu

2565 2330 234.5 234.5 216 212 203 200.5 200.5 198.5 198.5 197.5 198.5 197.5

Score

Result

ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180

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 Usage by and for commercial
              (See http://www.isb-sib.ch/announce,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                357 YIVGAGVEAVTVSVSATSNGTESG-GAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                          416 TEAGGTSGTTTSSGAASGKA-----GTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTG 468
                                                                                                                                                                                                                                                                                                                                                                                                  7.1%; Score 182.5; DB 1; Length 5263;
36.7%; Pred. No. 0.092;
Live 15; Mismatches 60; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLUIAR LOCATION: Integral membrane protein (Potential).
-!- SIMILARITY: CONTAINS I GPS DOMAIN.
                                                                                                                                                                                                 POTENTIAL.
FIBROIN HEAVY CHAIN.
HIGHLY REPETITIVE.
INTERCHAIN (WITH LIGHT CHAIN).
                                                                                                                                                                                                                                                                           -> V (IN REF. 2).
; 8EE11D3A0A47440E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wilkinson-Sproat J.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YS89_CAEEL STANDARD; PRT; 3178 AA. 009624, 009625; Q969D4; 0100V-1995 (Rel. 32, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 14/pothetical protein ZK945.9 in chromosome II. ZK945.9/ZK945.10. Caenorhabditis elegans.
modified and this statement is not removed.
            entities requires a license agreement (S
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              523 AGSGAGAGSGAGAGYGAGA 541
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EMBL; Z48582; CAB70192.1; JOINED.
                                                                                                                                                                                                                                                                                        5263 AA; 391586 MW;
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                                                                     EMBL, V00094, CAA23432 1, EMBL, V00097, CAA23433 1, EMBL, X18459; CAA32076 1, EMBL, M35378; AAA27839.1, EMBL, AB017362; BAA33147.1, PIR; S01844, S01844.
                                                       EMBL; AF226688; AAF76983.1; -.
                                                                                                                                                                                                                                                                                                                                                    51; Conservative
                                                                                                                                                                                                                                                                                                                                      Similarity
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YS89_CAEEL
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1156 SGTTASGSGSSGGSSG-TGSDGVNSGKTTALNGDGTGSGTATTPGSHLGDGGSTSGSGD- 1213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.0%; Score 180; DB 1; Length 3178; 84.9%; Pred. No. 0.068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          344726 MW; F8239436D03666CD CRC64;
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                                    InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR0010636; M+channel_nlg.
InterPro; IPR000203; PKD_cys_rich.
Pfam; PF01825; Ion_trans; I.
Pfam; PF01825; GPS; I.
SWART; SM00303; GPS; I.
SWART; SM00308; LH2; I.
                                                                                                                                                                                                                                                                  POTENTIAL. POTENTIAL.
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EMBL; 248544; CAB70201.1; JOINED. WormPep; ZK945.9; CE25697.
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DOMAIN 266 1
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Matches
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Search completed: July 16, 2003, 17:47:30 Job time: 31.688 secs

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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroin heavy chain precursor (Fib-H) (H-fibroin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      360 GAGVEAVIVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419
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Fletschmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Gaps
                                                                                                                                                                                                                                                                                                       "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                            MEDLINE-9879587; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Elgimeler K., Gas S., Barry C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Krogh A., McHean J., Moule S., Murphy L., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Slston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.";
                                                                                                                                                                                                                                                                                                                   laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases. ,
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.2%; Score 183.5; DB 1; Length 778;
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Q -> H (IN REF. 2).
A -> T (IN REF. 2).
; DABZOFE58E4999E7 CRC64;
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EMBL; AE007103; AAK47026.1; ALT_INIT.
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TubercuList; Rv2634c; -.
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CONFLICT 51 51
CONFLICT 63 63
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63 63
274
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                                                                                                                                                                                                                  SEQUENCE FROM N.A.
 NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                          SUBFAMILY
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5263 AA.

PRT;

FBOH_BOMMO STANDARD; P05790; Q26379; Q17220; O1-NOV-1988 (Rel. 09, Created)

FBOH_BOMMO RESULT 14

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-94365842; PubMed-7916056; Mita K., Ichimura S., James T.C.; "Highly repetitive structure and its organization of the silk fibroin gene.";
                   Journal Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Cusacta; Metazoa; Arthropoda; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The DNA sequence of Bombyx mori fibroin gene including the 5' flanking, mRNA coding, entire intervening and fibroin protein coding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mita K., Ichimura S., Zama M., James T.C.; "Specific codon usage pattern and its implications on the secondary structure of silk fibroin mRNA.";
                                                                                                                                                                                                         MEDILINE-20130362; PubMed-10871375;
Zhou C.-Z., Confalonieri F., Medina N., Zivanovic Y., Esnault C.
Yang T., Jacquet M., Janin J., Duguet M., Perasso R., Li Z.-G.;
Frine organization of Bombyx mori fibroin heavy chain gene.";
Nucleic Acids Res. 28:2413-2419(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PARTIAL SEQUENCE FROM N.A. MEDIINE-79211211; Pubmed-455439; Traulimnco Y., Suzuki Y.; "Structural analysis of the fibroin gene at the 5' end and surrounding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 5179-5263 FROM N.A., AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-89094868; PubMed-3210244;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-168 FROM N.A. MEDLINE-80045039; PubMed-498286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Biol. 203:917-925(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mol. Evol. 38:583-592(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARTIAL SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isujimoto Y., Suzuki Y.;
Bombyx.mori (Silk moth)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell 18:591-600(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               surrounding regions."
Cell 16:425-436(1979)
                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                               Ditrysia;
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Page 11

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SUBFAMILY,
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P71933;
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                                                                GGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGT-TT 463
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         ISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTES
                              IFSKKLLVSFGSLVALASIPLIAISCGQT-NTDKSQQPGSGSSTSGGQSGTGLGS-GTTT
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                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

Li-Weber M., de Groot E.J., Schweiger H.G.;

"Sequence homology to the Drosophila per locus in higher plant nuclear DNA and in Acetabularia chloroplast DNA.";

Mol. Gen. Genet. 2093:1-7(1987).

-1- SIMILARITY: TO THE PERIOD CLOCK PROTEINS OF DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Biological rhythms; Repeat; Chloroplast.

DOMAIN 49 138 45 X 2 AA TANDEM REPEATS OF G-T. SEQUENCE 174 AA; 16878 MW; E6C06770E9DDCB5D CRC64;
                                                                                                                                                                                               01-0CT-1989 (Rel. 12, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Period clock protein (P230).
Acetabularia mediterranea (Mermaid's wine glass).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.3%; Score 188.5; DB 1
40.3%; Pred. No. 0.00075;
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(Rel. 39, Last sequence update)
                                                                                                SSGTGAGGAGS----GGPSGHASNAKIPG 488
                                                                                                                   117 SODSGARGIGSDSODSGARGIGSDSODSG
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Dasycladaceae; Acetabularia.
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053553;
30-MAY-2000 (
30-MAY-2000 (
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P12347;
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01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
Hyporhetical PE-EGRS family protein Rv2634c.
RV2634C OR MTZ712 OR MTCY441.04C.
Mycobacterium tuberculosis.
Bacteria, Actinobacteria, Actinobacteriade;
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                             Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-9892987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.T., Brosch R., Gas S., Bary C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krooph A., Moclean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 393:537-544(1998).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.2%; Score 185; DB 1; Length 1901; 37.8%; Pred. No. 0.02; Live 12; Mismatches 55; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1901 AA; 147627 MW; C7B1923D5D0146CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein; Repeat; Signal; Complete proteome.
SIGNAL
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv3508 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         778 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----TGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                629 GADNPTGIGGAGGTGGTGGAAGA 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RV3508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TubercuList; Rv3508; -.
InterPro; IPR000084; PE_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ProDom; PD001223; PE_region; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL022022; CAA17745.1; -.
                                                                                                                         Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                               Hypothetical PE-PGRS
RV3508 OR MTV023.15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00934; PE;
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=1773;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                              281 KAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKI 340
                                                                               -----GEGSSSGGGGRRG-----GS 467
                                                      341 N-RDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGN 399
                                                                                                            GGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTS 459
                         388 ASLAETEGRYCVQLSQIQSQISALEEQLQQIRAETECQNAEYQQLLD------IKT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Probable).
MISCELLANEOUS: THE NUMBERS OF REPEATS CAN VARY AND IS ONE OF THE
BASIS OF THE ANTIGENIC DIVERSITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADAPTATION.
-1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDELINE-22097525; PubMed=1721868;
Yogev D., Rosengarten R., Watson-Mckown R., Wise K.S.;
"Molecular basis of Mycoplasma surface antigenic variation: a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            set of divergent genes undergo spontaneous mutation of periodic coding regions and 5 regulatory sequences."; EMBO J. 10:4066-4079(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-ACYL DIGLYCERIDE (PROBABLE). 7 X 12 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                             01-DEC-1992 (Rel. 24, Created)
1-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Variant surface antigen B precursor (VLPB prolipoprotein).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lipoprotein; Repeat; Signal.
29 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7.4%; Score 190.5; DB 1
35.6%; Pred. No. 0.00058;
ive 25; Mismatches 58
                                                                                                                                                                                                                                                                    174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; S18654; S18654.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                                             521 GGSSSGGAGGHGGSSGGGYGGGSSS 545
                                                                                                                                                                    GTTTSSGTGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X62936; CAA44709.1; ALT_SEQ.
                                                                               438 RLENEIQTYRSLLE------
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                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    Mycoplasma hyorhinis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       174 AA;
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Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-2100;
                                                                                                                                                                                                                                                                  VLPB_MYCHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYE---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EADI-NGLRRVLDEL-----TLSKSDLEMQIESLNEELAYLKKNHEEEMRDLQNVSTGD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       299 VNVEMNAAPGVDLTQLLNNMRNQ----YEQLAEKNRKDAEEWFNQKS------
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OSVLEL (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%; Score 192; DB 1; Length 569;
22.0%; Pred. No. 0.002;
tive 68; Mismatches 192; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  X -> G (IN REF. 2).
S -> G (IN REF. 2).
G -> R (IN REF. 2).
WEEKHGNSGO -> VYRERROLKP (IN R KSDLEM -> GYLLL (IN REF. 2).
H -> L (IN REF. 2).
E -> A (IN REF. 2).
EGRYCV -> VESLLR (IN REF. 2).
EGRYCY -> VESLLR (IN REF. 2).
GGSHGGG -> GGGRGGG (IN REF. 2).
H -> R (IN REF. 2).
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S -> G (IN REF. 2).
GQ -> RR (IN REF. 2).
KS -> SGT (IN REF. 2).
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S -> F (IN REF. 2).
S -> F (IN REF. 2).
Y -> L (IN REF. 2).
E -> G (IN REF. 2).
AG -> GS (IN REF. 2).
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(IN REF. 2).
(IN REF. 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                         MISSING (IN REF
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PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin.
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GLY/SER-RICH.
email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                              LINKER 12.
                                                                                                                                                                                                                                                       COIL 1A.
LINKER 1.
                                                                                                                                                                                                                                                                                   COIL 1B.
                          EMBL; L00193; AAA39391.1; -.
EMBL; M10081; AAA39391.1; JOINED.
EMBL; V00830; CAA24214.1; -.
                                                                PIR: A02940; KRWSEI.
PIR: S07330; S07330; MGD; MG196668; KrL1-10.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57711 MW;
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                                                                                                                                           filament;
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                                                                                                                                       Pfam; PF00038;
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CONFLICT
CONFLICT
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NCBI_TaxID=10090;
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SEQUENCE
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                                                                                                                                       IYHTISSQ---ISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN 185
                                                                                                                                                             439 TYETVMKKGQTAGASFCSKPYRFLIQNGCYVL-LETEWTSFVNPWSRKLEFVVG----HH 493
                                                                                                                                                                                    NMFQ------EALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG 237
                                                                                                                                                                                                                                              SGASGPMSP-VHEGSGGSGSSGNFTTASNIHMSSVTNTSIAGTG-----GTGTGTGTG 705
                                                                                                                                                                                                                                                                                                                                                                                      PHHDYYDSKSST - - - ETPPSYNQLNYNENLLRFFNSKPVTAPAELDPPKTEPPEPRGTCV 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SHSWEGEANKPKQQLTLGTDAIKGAAGSAGGAVGTGGVGGGGGGGGAGV-AGGGGGGGTLGTDAIKGAAGSAGGAVGTGGVGGGAGV-AGGGGGGGTLGTP 884
                                                                                                                                                                                                  GEVTSNFRY ISKEY EYEHTEL - - - - - AKEHCKKEKCVNVDNI EDNNLK IYAKQFKSVVT
                                                                   GLKSGGFGVIGRPVSYEPFRLGLTFREAPEEARPDNYM-VSNGTNMLLVICATPIKSSYK
                                                                                            ---QPNTVGMSLEQFIKNELYSFSNE
                                                                                                          NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTE
                                                                                                                                                                                                                                238 YDFDYINTKKELV----ILASVLDGL-----DLIMERLIENFSDVNNTDDIKKA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --------GAASGKAGTGTAGTTTTSSEGAGSDKAGTGTSGT-
                                                                                                                                                                                                                                                                                                                                                                         SG-GAGSGTGTSV-SATSTLTGNG-GTESGGTAGTTTSSGTEAGGTSGTTTSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                          766 PPVTLTESLLNKHNDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGG
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;uli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bohne W., Ferguson D.J.P., Kohler K., Gross U.;
Bohne W., Ferguson D.J.P., Kohler K., Gross U.;
"Molecular characterisation of a developmentally expressed spore protein from the human microsportidian Encephalitozoon cuniculi."
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
 Length 1224;
                         Indels
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Eukaryota, Microsporidia, Unikaryonidae, Encephalitozoon.
                                                                                                                                                                                                                                                                               ----FDECKSNAIILKKKILDNDEDYKINFREMVNEV-----
 DB 1;
                      220;
7.7%; Score 196.5; DB 21.7%; Pred. No. 0.0029 iive 69; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Rel. 39, Created)
(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
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                                                                                           TPADV-AGVSDGFFIRGONLGAVGSVNE-----
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                        Conservative
            Similarity
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30-MAY-2000
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                      136;
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  Query Match
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                 (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between the Swiss Institute of Bioinformatics and the EMBL outstation-
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                         315 VTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATS 374
                                                                                                                                                                                                                                                                                                                                                                                                                                    287 ITAITNALQANKNNFVTFFTTQTTNLQTDVQNALTALITALTTLTS-----TTSTEFTQ 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 -----NGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        426 TSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASN 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        p02535; p08731;
21-0701-1986 (Rel. 01, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (56 kDa cytokeratin)
(Keratin, type I cytoskeletal 59 kDa).
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                               23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-85207552; PubMed-2581944;
Krieg T.M., Schafer M.P., Cheng C.K., Filpula D., Flaherty P.,
Steinert P.M., Roop D.R.,
"Organization of a type I keratin gene. Evidence for evolution
                                                                                                                                                                                                                                                                                                    DB 1; Length 450;
                                                                                                                                                                                                                                                                                                                                               Indels
Usage by
                                                                                                                                                                                                                                                           5E7071A3E3A6DF60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                termediate filaments from a common ancestral gene."; Biol. Chem. 260:5867-5870(1985).
                                                                                                                                                                                                                                                                                  7.5%; Score 193.5; DB 1; 28.7%; Pred. No. 0.0013; Mismatches 64;
                                                                                                                                               SPORE WALL PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA
modified and this statement is not removed.
                                                                                                                                                                                                                                       GLY/SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         569
                    entities requires a license agreement (Son send an email to license@isb-sib.ch).
                                                                                                                                                                        POLY-SER.
                                                                                                                                                                                            POLY-ARG.
                                                                                                                                                                                                                   THR-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rođentia;
                                                                                                                                                                                                                                                         45873 MW;
                                                                                EMBL; AJ133745; CAB39735.1;
                                                                                                                                                                                                                                                                                                                                               51; Conservative
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                                                                                                                           18
450
74
82
339
450
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79
303
355
450 AA;
                                                                                                                                                                                                                                                                                                                          Similarity
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BEHAVIOR.
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PHOSPHORYLATION
RAPELINE=9418172; Pubmed=8134384;
RA MEDILINE=94181572; Pubmed=8134384;
RT MEDILINE=94181572; Pubmed=8134384;
RT Temporal phosphorylation of the Drosophilal period protein.";
Proc. Natl. Acad. Sci. U.S.A. 91:2260-2264(1994).
LT-COC. Natl. Acad. Sci. U.S.A. 91:2260-2264(1994).
RHYTHAIC COMPONENT OF THE MALE COURTSHIP SONG THAT URCREASE IN RHYTHMIC COMPONENT OF THE MALE COURTSHIP SONG THAT ORIGINARES IN THE THORACIC NERVOUS SYSTEM. THE BIOLOGICAL CYCLE DEPENDS ON THE RHYTHMIC COMPONENT OF THE MALE COURTSHIP SONG THAT TORICINARES IN THE THORACIC SYSTEM. THE BIOLOGICAL CYCLE DEPENDS ON THE RHYTHMIC COMPONENT OF THE MALE COURTSHIP SONG THAT THE TIM-PER COORDINATIVE REGULATES PER AND THM TRANSCRIPTION THROUGH A NUGATIVE REGULATES PER AND THM TRANSCRIPTION THROUGH A NUGATIVE RESULATES PER AND THE TIM-PER COORDINATIVE TRANSCRIPTIONAL LOOP. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN SUGGESTING
TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING
TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING
TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING
TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND DNA, SUGGESTING
TRANSCRIPTIONAL LOOP. DOES NOT APPEAR TO BIND SOUTH DOT SET RENAULATES IN THE PERRINDCENS: RESION ABOUT ONE HORR BEFORE
TRANSCRIPTIONAL LOCATION: NUCLEUS. INTERESTION WITH TIM IS REQUIRED
TRANSCRIPTIONER SPLICIUS.
TRANSCRIPTIONER SPLICIUS INDEPRODERS AND IN SEVERAL
TISSUE SPECIFICITY: EXPRESSED IN NEURBAL TISSUES ON THE BRAIN.
THERE), PER-A/SHORT, PER B, PER-C, PER-D AND PER-E; ARE PRODUCED BY ALTERNATIVE SPLICES IN ABDOMENT ON BALDEGHMENT OF THE BRAIN.

TISSUE SPECIFICITY: EXPRESSED IN ADULT'S HEAD.

TISSUES OF THE REPORT THAT THE TRANSCRIP OF THE BRAIN.

TISSUES SPECIFICITY: EXPRESSED IN ACTIONS STUDIED EXCEPT FOR THE OVARY.

THERE THE STORE THAT THE STORE STUDIED E STRAIN-Oregon-R;
MEDLINE-86545055; PubMed-3087625;
REddy P., Jacquier A.C., Abovich N., Petersen G., Rosbash M.;
Reddy P., Jacquier A.C., Abovich N., Petersen G., Rosbash M.;
The period clock locus of D. melanogaster codes for a proteoglycan.";
Cell 46:53-61(1986). SEQUENCE OF 63-573 FROM N.A. (ISOFORM PER-A).
MEDLINE-93170641; PubMed-8436278;
Kliman R.M., Hey J.;
"DNA sequence variation at the period locus within and among species of the Drosophlia melanogaster complex."; SEQUENCE OF 499-1075 FROM N.A. (ISOFORM PER-A) Science 287:2220-2222(2000). melanoqaster.";

DOMAIN: CONTAINS A REMARKABLE RUN OF ALTERNATING GLY-THR RESIDUES WHICH IS POLYMORPHIC IN LENGTH. AT LEAST THREE TYPES OF GLY-THR LENGTH EXIST IN THE NATURAL POPULATION, (GLY-THR)23 (SHOWN HERE), AND TWO MAJOR VARRANTS (GLY-THR)17 AND (GLY-THR)20. THIS GLY-THR STRETCH IS IMPLICATED IN THE MAINTENANCE OF CIRCADIAN PERIOD AT BIFFERENT TEMPERATURES. DELETION OF THE REPEAT LEADS TO A SHORTENING OF THE COURTSHIP SONG CYCLE PERIOD, AND THUS COLLD BE IMPORTANT FOR DETERMINING FEATURES OF SPECIFS-SPECIFIC MATING

AVSDPCKKEVPDSSPIPSVMGDYNSDPPCSSSNPANNKKYT DSNGNSDDMDGSSFSSFYSSFIKTTDGSESPPDTEKDPKHR

TTPASMTKKVPGAFHSVTTPAQVQRPSSQSASVKTEPGSSA

REGULATES THE RHYTHM OF SPECIES-SPECIFIC

COURTSHIP

POLY-GLY. POLY-GLY. POLY - ALA POLY-ALA POLY - ALA

879 905 914 1013 1041 868

DOMAIN DOMAIN MISSING (IN ISOFORM PER-A/SHORT). MISSING (IN ISOFORM PER-B). MISSING (IN ISOFORM PER-D AND ISOFORM

62 963 958

VARSPLIC VARSPLIC 1224

VLTPTPTPYSSIDHAGVHDEEGAGCIPLGHHSCPGAASLLA ERIRQDGAGLQCSGIRSLQEGGAGLLAHSLRDGRLQLRPAL

KLKSMSTSESKIMEHPEEDQTQHGDG -> VSQWPVVPHRT

KYTDSNGNSDDMDGSSFSSFYSSFIKTTDGSESPPDTEKDP KHRKLKSMSTSESKIMEHPEEDQTQHGDG -> VCYTNEVH

W (IN ISOFORM PER-E)

MISSING (IN (GLY-THR)20).
MISSING (IN (GLY-THR)17).
G -> V (IN REF. 6; AAA28777).
E -> A (IN REF. 5; AAA28777).
T -> S (IN REF. 5).
T -> S (IN REF. 15).

702 708 211 499 637 762

VARIANT CONFLICT CONFLICT CONFLICT CONFLICT

QQQQSRQQQGMLYE (IN ISOFORM PER-C)

VARSPLIC

VARIANT

DOMAIN: MUTATIONS IN THE PAS DOMAIN RESULT IN LONGER CIRCADIAN RHYTHMS AND COURTSHIP SONG (PERL MUTATION) OR MAKES THE FLIES ARRHYTHMIC (PEROI MUTATION).

PTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER PER-TIM.

SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
DATABASE: NAME-PROTEIN Spotlight;
NOTE-ISSUE 6 of January 2001;

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56 79 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
57 297 PAS 1.
77 447 PAS 2. WWW-"http://www.expasy.org/spotlight/articles/sptlt006.html". Nuclear protein; Phosphorylation; REPEATS POLY-GLU. POLY-ALA. POLY-LYS G-T InterPro; IPR001610; PAC. InterPro; IPR000014; PAS_domain. Pfam; PF00989; PAS; 2. X03636; CAA27285.1; -. AL024485; CAA19677.1; -. AL024485; CAA19678.1; -. AL024485; CAA19679.1; -. AL024485; CAA19680.1; -. D00009; BAA00007.1; -. EMBL; M30114; AAA28752.1; -. M30114; AAA28754.1; -. AF033029; AAB87476.1; M30114; AAA28753.1; -. L07825; AAA28769.1; -. PROSITE; PS50112; PAS; 2. Biological rhythms; Repeat; AAA28777.1; -AAA28775.1; -AAA28773.1; -L07823; AAA28771.1; AAA28776.1; FlyBase; FBgn0003068; per SMART; SM00086; PAC; 1 SMART; SM00091; PAS; 2 PIR; A23932; UMFF L07818; L07819; L07821; Polymorphism; L07817 DOMAIN EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL; EMBL: EMBL; EMBL; EMBL; EMBL; EMBL;

141. 141 141 AA; 12325 MW; E407A197912E3AE2 CRC64;

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NON_TER
SEQUENCE
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-1- SUBBNIT: FORMS HETERODIMER WITH TIMELESS (TIM); THE COMPLEX THEN TRANSCRIPTIONAL LOOP. DES NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT TRANSCRIPTIONAL INHIBITION (BY SIMILARITY).

-1- SUBGELLULAR LOCATION NUCLEAR REGION ABOUT ONE HOUR BEFORE FIRST ACCUMULARES IN THE BERINUCLEAR REGION ABOUT ONE HOUR BEFORE THE MALL AND THE NUCLEAR REGION ABOUT ONE HOUR BEFORE THE WASHELD ON THE LIB NUCLEAR REGION MITH TIM IS REQUIRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
518 SMSGSSSRGGSGGGR----YGGGGSYGGG----SGGGSYGGSSGGGSGGSYG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR NUCLEAR LOCALIZATION (BY SIMILARITY).

DOMAIN: THE RUN OF GLY-THR IS IMPLICATED IN THE MAINTENANCE OF CIRCADIAN PERIOD AT DIFFERENT TEMPERATURES. DELETION OF THE REPEAT LEADS TO A SHORTENING OF THE COURTSHIP SONG CYCLE PERIOD, AND THUS COULD BE IMPORTANT FOR DETERMINING FEATURES OF SPECIES-SPECIFIC MAING BEHAVIOR (BY SIMILARITY).

PHY: PHOSHORYLAND WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: ESSENTIAL FOR BIOLOGICAL CLOCK FUNCTIONS. DETERMINES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER
                                                                                                                                                                                                                                                                        Drosophila serrata (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBL_raxID=7274;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-93196482; PubMed-8450754;
Peixoto A.A., Campesan S., Costa R.H., Kyriacou C.P.;
"Molecular evolution of a repetitive region within the per gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biological rhythms; Repeat; Nuclear protein; Phosphorylation.
NON_TER 1 1
                                  433 GKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGG 476
                                                     01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                          141 AA
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POLY-SER.
                                                                                                                                                                                                                                             Period circadian protein (Fragment)
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121
128
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Mol. Biol.
                                                                                                                                                        PER_DROSR
Q04537;
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                                                                                                                                         369 SVSATSNGTESGGAGSGTGTSVSATSTLTGNG-GTESGGTAGTTTSSGTEAGGTSGTTTS 427
                                                                                                                                                                                     "A family of unusually spliced biologically active transcripts encoded by a Drosophila clock gene.";
Nature 326:42-47(1987).
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baylies M.K., Weiner L., Vosshall L.B., Saez L., Young M.W.; "Genetic, molecular and cellular studies of the period locus and its products in Drosophila melanogaster.";
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Benos P.V. Gatt M.K., Ashburner M., Murphy L., Harris D.,
Barrell B.G., Ferraz C., Videl S., Brun C., Demailles J., Cadieu E.,
Barrell B.G., Ferraz C., Videl S., Brun C., Demailles J., Cadieu E.,
Breano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
Papagajannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
Beinert N., Dowe G., Schoettler P., Werner M., Mourkioti F.,
Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
Glover D.M.;
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Molecular genetics of biological rhythms, pp.123-153, Marcel Dekker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Colot H.V., Jacquier A.C., Yu Q., Hall J.C., Baltimore D.,
                                                                                                                                                                                                                                                                                   428 SGAASGKA-GTGTA-GTTTSSEGAGSDK-AGTGT-SGTTTSSGTGAGGAGSGGP 477
                                                                                                                                                                                                                                                                                                                    PER_DROME STANDARD; PRT; 1224 AA.
P07663; 017483; Q24446; Q24447; Q24448; Q24449; O76882; O76883; O76884; O76885;
O1-APR-1988 (Rel. 07, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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Length 141;
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                                                                        Indels
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Jackson F.R., Bargiello T.A., Yun S.-H., Young M.W.;
"Product of per locus of Drosophila shares homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Period circadian protein (Clock-6 protein) (CLK-6).
Score 199.5; DB 1
Pred. No. 0.00015;
                                                                    16; Mismatches
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   7.8%;
                             Similarity 49.18;
                                                                    56; Conservative
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Nature 320:185-188(1986).
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   Query Match
Best Local 3
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"Amino acid sequences of mouse and human epidermal type II keratins of Mr 67,000 provide a systematic basis for the structural and functional diversity of the end domains of keratin intermediate finament subunits.": 1 Biol. Chem. 260:7142-7149(1985) 2 Biol. Chem. 260:7142-7149(1985) 2 Biol. Chem. 260:7142-7149(1985) 2 Biol. Chem. 260:7142-7149(1985) 2 Biol. Chem. 260:7142-7149(1985) 3 Biol. Chem. 260:7142-7149(1985) 4 Computed (Jan-1999) to the EMBL/GenBank/DDBJ databases 3 Computed (Jan-1999) to the EMBL/GenBank/DDBJ databases 4 Computed (Jan-1999) to the EMBL/GenBank/DDBJ databases)	This bett the the use mod mod or sor	REMBL; M10937; AAD05191.1; - REMBL; M10937; RAM25. RAD251; RRM22. REMISS-2DPAGE; P04104; MOUSE. RGD; MG1:96698; Krt2-1. RGD; MG1:96698; Krt2-1. RGD; MG1:96698; Krt2-1. REMCD: MG1:96698; Krt2-1. REMCD: MG1:96698; Krt2-1. RGD; RGD; RGD; RGD; RGD; RGD; RGD; RGD;	DOMAIN 334 357 DOMAIN 358 496 SITE 451 451 SEQUENCE 627 AA; 65092 MW; QUELY MATCH 7.8%; Best Local Similarity 21.3%; Matches 99; Conservative 61 150 VKHDNYILKKEGEGCEQIYN 174 VKVDPQIQKVKSGEREQIKS 185 NNWFQEALIRFRNASSEEWIK 234 LDPFFENYISILRRKVDSLK	245 TKKELVILASVLDGL
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329 329 357 357 489 489 536 536 559 565 632 632	Query Match 8.1%; Score 209; DB 1; Length 643; Best Local Similarity 22.6%; Pred. No. 0.0029; Matches 119; Conservative 74; Mismatches 162; Indels 172; Gaps 24; Qy 85 GVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIRNELYSFSNEIYHTISSQ 136	184 KSLNNOFASFIDKVRFLEQQNQVLQTKWELLQQVDTSTRTHNLEPYFESFINNLRRRVDQ 179GARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNF 1 1 1 1 1 1 1 1 1	Qy 319 NTREE-ALNDLI	RESULT 5 K2C1_MOUSE TO ACC1_MOUSE TO POUTON TO 1-NOV-1986 (Rel. 03, Created) TO 1-NOV-1986 (Rel. 03, Created) TO 1-NOV-1986 (Rel. 40, Last sequence update) TO 1-NOV-1986 (Rel. 40, Last annotation update) TO 1-OCT-2000 (Rel. 39, Last sequence update) TO 16-OCT-2001 (Rel. 40, Last annotation update) TO NEW RT2-1. ON KRT2-1. ON MRMmalla; Eutheria; Rodentia; Craniata; Vertebrata; Buteleostomi; OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; OC Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Muslinae; Mus. NO NOBLITE-200740; PubMed-2581964; RM Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C., RA Roop D.R.;

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SEQUENCE FROM N.A. Hatsell S.J., Eady R.A., Wennerstrand L., Dopping-Hepenstal P., Leigh I.M., Munro C., Kelsell D.P.; "Novel splice site mutation in keratin I underlies mild epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92376531; PubMed-1380725; Rothnagel J.A., Dominey A.M., Dempsey L.D., Longley M.A., Greenhalgh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.; "Mutations in the rod domains of keratins 1 and 10 in epidermolytic
20-MAR-1987 (Rel. 04, Created)
1-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-STAN-2001 (Rel. 10 those the sequence of the sequen
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MEDLINE-85207740; PubMed-2581964;
Steinert P.M., Parry D.A.D., Idler W.W., Johnson L.D., Steven A.C.,
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MEDLINE-94117869; Pubmed-7507151;
Yang J.-M., Chipev C.C., Digiovanna J.J., Bale S.J., Marekov L.N.,
Steinert P.M., Compton J.G.;
"Mutations in the H1 and IA domains in the keratin 1 gene in
epidermolytic hyperkeratosis.";
                                                                                                                KRT1 OR KRTA.
Homo saptens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
Morley S.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Mutations in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE).";
J. Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "A leucine-->proline mutation in the H1 subdomain of keratin 1 causes epidermolytic hyperkeratosis."; Cell 70:821-828(1992).
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE-81166239; PubMed=2580302;
Johnson L.D., Idler W.W., Zhou X.-M., Roop D.R., Steinert P.N.
"Structure of a gene for the human epidermal 67-kDa keratin."
Proc. Natl. Acad. Sci. U.S.A. 82:1896-1900(1985).
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Wilton Wilton N.A.; Miltock N.V., Eady R.A., McGrath J.A.; Menomic organization of the human keratin 1 gene."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         palmoplantar keratoderma in three kindreds.";
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases
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VARIANTS EHK PRO-185 AND SER-187.
MEDLINE-94117870; PubMed-7507152;
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[9]
VARIANT ALLELE 1B.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                          PORESKIN. THE 67-KDA TYPE II KERATINS ARE EXPRESSED IN TERMINALLY DIFFERENTATING EPIDERMIS.

POLYMORPHISM: THERE ARE TWO SIZE VARIANTS OF KRT1, TERMED IA AND 1B WITH ALLELIC FREQUENCIES OF 0.61 AND 0.39. 1B LACKS 7 LACKS 7 RESIDUES COMPARED TO 1A.

DISEASE: DEPECTS IN KRT1 ARE A CAUSE OF EPIDERMOLYTIC HYPERKERATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL ICHTHYOSIFORM EXYTHRODERMA (BIE)); A HEREDITARY SKIN DISORDER CHARACTERIZED BY BLISTERING AND A MARKED THICKENING OF THE STRATUM
                                             to a deletion in the
                    Korge B.P., Compton J.G., Steinert P.M., Mischke D.;
The two size allales of human keratin I are due to a deletion in t
glycine-rich carboxyl-terminal V2 subdomain.";
J. Invest. Dermatol. 99:697-702(1992).
-!- SUBGNIT: HETERORETRAMER OF TWO TYPE I MOD TYPE II KERATINS.
KERATIN I IS GENERALLY ASSOCIATED WITH KERATIN 10.
-!- TISSUE SPECIFICITY: THE SOURCE OF THIS PROTEIN IS NEONATAL
                                                                                                                                                                                                                                                                                                                                                                                                                                       MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND (NEUTRAL TO BASIC; 56-70 kDa) [K1 TO K8].
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT.FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
Polymorphism; Phosphorylation.
INTT_MET 0 0 BY SIMILARITY.
DOMAIN 1 178 HEAD
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V -> G (IN EHK).
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L -> P (IN EHK).
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/FIId=VAR_003857
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LINKER 1.
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EMBL; M98776; AAB47721.1;
EMBL; MF304164; AAA31547.1; --
EMBL; M10938; AAA3153.1; ALT_SEQ.
PIR; A02950; KRHU2.
PIR; A22940; A22940.
Aarhus/Ghent-2DPAGE; 4606; NEPHGE.
Genew, HGNC: 6412; KRT1.
MIN; 139360; --
MIN; 113800; --
MEDLINE-93107743; PubMed-1281859;
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InterPro; IPR003054; Keratin_II.
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K2C1_HUMAN STANDARD P04264; Q14720; Q9H298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIEMENS (1BS), A RARE AUGSOMAL DOMINANT DISORDER DISPLAYING A SIEMENS (1BS), A RARE AUTOSOMAL DOMINANT DISORDER DISPLAYING A SIEMENS (1BS), A RARE AUTOSOMAL DOMINANT DISORDER DISPLAYING A STEEMING FROM BIRRH. HYPERKERATOSES AND SHEDDING OF THE OUTER LAYERS OF THE EPIDERMIS (MOLTING) ARE OBSERVED IN LATER WEEKS. MISCELLANBOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBALLAR KRATIN: I (ACIDIC, 40-55 kDa) [K9 TO K20] AND II (NEUTRAL TO BASIC; 56-770 kDa) [K1 TO K8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEVELOPMENTAL STAGE: SYNTHESIZED DURING MATURATION OF EPIDERMAL KERATINOCYTES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- FUNCTION: PROBABLY CONTRIBUTES TO TERMINAL CORNIFICATION.
-i- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
-i- TISSUE SPECIFICITY: IN THE SUPRABASAL LAYERS OF EPIDERMAL
TISSUES FROM MOST BODY SITES, EXCEPT IN FORESKIN, IN SQUAMOUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
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COIL 1A.
LINKER 1.
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[5]
VARIANTS IBS ASP-493 AND LYS-493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003054; Keratin_II.
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PRINTS; PR01276; TYPE2KERATIN.
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MIM; 146800;
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                                                                                                                                                    SIMILARITY).
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EE025A173E33409A CRC64;
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N - D (IN IBS).

N TIG-VAR_010515.

N - Y (IN IBS).

FTIG-VAR_009185.

E -> K (IN IBS).

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/FTIG=VAR_009187.
L -> P (IN IBS).
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E -> D (IN IBS).
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COllin C., Moll R., Kubicka S., Ouhayoun J.-P., Franke W.W.;
"Characterization of human cytokeratin 2, an epidermal cytoskeletal protein synthesized late during differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e)
    244 LRQSVEADI----NGLRRVLDELTLTKADLEMQIESLTEELAYLKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND VARIANTS IBS TYR-192 AND LYS-482.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TGTSGTTTSSGTGAGGAGSGGPSGHASNA 484
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MEDLINE-94358461; PubMed=8077693;
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Invest. Dermatol. 111:817-821(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cell_Res. 202:132-141(1992).
                                               173 FIEKLRGARSEGNNMFQEA----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
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KRT2A OR KRT2E.
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burdean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             138 DGGLLSGNEKVTMONLNDRLASYLDKVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYS 197
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  MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND II
           (NEUTRAL TO BASIC; 56-70 kDa) [KI TO K8].
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY
POSITIONS 513 TO 555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 593;
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/FTId=VAR_003826.

R -> H (IN EHK).

/FTId=VAR_003827.

R -> C (IN EHK).
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/FTId=VAR_010506.
M -> T (IN EHK).
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Pred. No. 9.5e-05;
; Mismatches 207
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FFIId=VAR_003829.
R -> S (IN EHK).
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/FTId=VAR_003830.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002957; Keratin_I. Pfam; PF00038; filament; 1. PRINTS; PR01248; TYPE1KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-2DPAGE; P13645; HUMAN.
Aarhus/Ghent-2DPAGE; 7405; IEF
Genew; HGNC:6413; KRT10.
                                                                                                                                                                                                                                                                                                          EMBL; X14487; CAA32649.1; -.
                                                                                                                                                                                                                                                                                                                              M19156; AAA59468.1; -. M77663; AAA59199.1; -. L20218; AAB59438.1; -. L20219; AAB59439.1; -.
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MIM; 113800;
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MEDLINE-94136477; PubMed-7508181;
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  Korge B.P., Gan S.-Q., McBridge O.W., Mischke D., Steinert P.M.; "Extensive size polymorphism of the human keratin 10 chain resides in the C-terminal V2 subdomain due to variable numbers and sizes of 91ycine loops.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rothnagel J.A., Dominey A.M., Dempsey L.D., Longley M.A., Greenhalgh D.A., Gagne T.A., Huber M., Frenk E., Hohl D., Roop D.R.; "Mutations in the rod domains of keratins 1 and 10 in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIANE-88122104; PubMed-2448602;
Darmon M.Y., Semat A., Darmon M.C., Vasseur M.;
"Sequence of a cDNA encoding human keratin No 10 selected according
to structural homologies of keratins and their tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vandekerckhove J.; "Microsequences of 145 proteins recorded in the two-dimensional gel
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                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                    Rieger M., Franke W.W.;
"Identification of an orthologous mammalian cytokeratin gene. Hig degree of intron sequence conservation during evolution of human cytokeratin 10.";
J. Mol. Biol. 204:841-875/1988)
                                                                                                                                              01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (K10) (CK 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             *Exons I and VII of the gene (Kerl0) encoding human keratin 10 undergo structural rearrangements within repeats.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein database of normal human epidermal keratinocytes.";
Electrophoresis 13:960-969(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 89:910-914(1992)
                                                                                   593 AA.
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANTS.
MEDLINE=92141228; PubMed=1371013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANTS EHK HIS-156 AND SER-161.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-92386600; PubMed-1381287;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-93162043; PubMed=1286667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mol. Biol. 204:841-856(1988).
                                                                                                                            01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 130-593 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Science 257:1128-1130(1992).
                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gene 116:245-251(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Keratinocytes;
                                                                                                                                                                                                                                      Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expression.
                                                                                 K1CJ_HUMAN
P13645;
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                                      RESULT 2
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-!- POLYMORPHISM: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN THE GLY-RICH REGION (POSITIONS 490-560).
-!- DISEASE: DEFECTS IN KRT10 ARE THE CAUSE OF EPIDERMOLYTIC HYPERKERATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL ICHTRYCSIEORE REYTHRODERMA (BCIE)); A HERBITARY SKIN DISORDER CHARACTERIZED BY BLISTERING AND A MARKED THICKENING OF THE STRATUM CORNEDW. AT BIRTH, AFFECTED INDIVIDUALS USUALLY PRESENT WITH REDWESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS. WITHIN A FEW WEEKS, THE ERYTHRODERMA AND BLISTER FORMATION DIMINISH AND HYPEKKERATOSES DEVELOP. TRANSMISSION IS AUTOSOWALD DOMINNAT, BUT MOST CASES ARE SPORADIC.
-!- DISEASE: DEFECTS IN KRT10 ARE THE CAUSE OF ANNULAR EPIDERMOLYTIC ICHTHYOSIS (AEI), A DISTINCT PHENOTYPIC VARIANT OF EPIDERMOLYTIC HYPERKERATOSIS. IT RESEMBLES CLINICAL AND HYSTOLOGIC FEATURES OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arin M.J., Longley M.A., Anton-Lamprecht I., Kurze G., Huber M.,
Hohl D., Rothnagel J.A., Roop D.R.;
A novel substitution in keratin 10 in epidermolytic hyperkeratosis.";
J. Invest. Dermatol. 112:506-508(1999).
-!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
KERATIN IO IS GENERALLY ASSOCIATED WITH KERATIN 1.
-!- TISSUE SPECIFICITY: SEEN IN ALL SUPRABASAL CELL LAYERS INCLUDING
STRATUM CORNEUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRATUM
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MEDLINE-95059228; PubMed-7526210;
Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
                                                                                                                                                                                                                                        VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126. MEDLINE-94216497; PubMed-7512983; Syder A.J., Yu Q.-C., Paller A.S., Giudice G., Pearson R., Fuchs E.; "Genetic mutations in the Kl and Kl0 genes of patients with epidermolytic hyperkeratosis. Correlation between location and disease severity."; J. Clin. Invest. 93:1533-1542(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R., Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
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Chipev C.C., Yang J.-M., Digiovanna J.J., Steinert P.M., Marekov L., Compton J.G., Bale S.J.,
"Preferential sites in Keratin 10 that are mutated in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT EHK ASN-160.
MEDLINE-A4117868; Pubmed-7507150;
Rothnagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.;
"Prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Watetions in the rod 1A domain of keratins 1 and 10 in bullous congenital ichthyosiform erythroderma (BCIE)."; Invest. Dermatol. 102:24-30(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genetic and clinical mosaicism in a type of epidermal nevus.";
New Engl. J. Med. 331:1408-1415(1994).
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MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDILINE-99072665; PubMed-9856845;
Suga Y., Duncan K.O., Heald P.W., Roop D.R.;
"A novel helix termination mutation in keratin 10 in annul
epidermolytic ichthyosis, a variant of bullous congenital
ichthyosiform erythroderma.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequencing.";
J. Invest. Dermatol. 102:13-16(1994).
                                                                                                                                                                          Am. J. Hum. Genet. 54:179-190(1994).
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MEDLINE-94117870; Pubmed-7507152;
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                                                                                                                                            hyperkeratosis.";
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:37:24 ; Search time 29.688 Seconds (without alignments) 702.728 Million cell updates/sec Run on:

US-09-853-079-52
2565
1 RRFNEHTDMNGIHYYYIDGS.....AKIPGIMTLTLFALLTFIVN 503 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description.	snm 6	homod		homo	mus m	_		Q9xzv1 encephalito		_	347	053553 mycobacteri	933		Q09624 caenorhabdi	P46591 candida alb		P03211 epstein-bar			Q03353 drosophila	006794 mycobacteri			Q03293 drosophila	P35527 homo sapien	_	P08673 plasmodium		P29228 mycoplasma	58 equin	3647 homo	Q01546 homo sapien
SUMMARIES		ΠD	PHX5_MOUSE	K1CJ_HUMAN	K22E_HUMAN	K2C1_HUMAN	K2C1_MOUSE	PER_DROSR	PER_DROME	SWP1_ENCCU	K1CJ_MOUSE	VLPB_MYCHR	PER_ACEME	YZ08_MYCTU	YQ34_MYCTU	FBOH_BOMMO	YS89_CAEEL	HYR1_CANAL	YA68_MYCTU	EBN1_EBV	CYS4_DICDI	K1CJ_BOVIN	PER_DROMA	WA22_MYCTU	Y747_MYCTU	SPG7_DICDI	PER_DROAN	K1CI_HUMAN	FSH_DROME	CSP_PLACC	APMU_PIG	VLPA_MYCHR	VGLX_HSVEB	K2C5_HUMAN	K220_HUMAN
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		Score	222	217.5	217	209	201	199.5	196.5	193.5	192	190.5	188.5	185	183.5	182.5	180	176.5	17.6	176	175	174	172.5	171.5	166.5	165	164.5	164.5	164.5	163.5	163.5	163	162.5	161	161
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RTOA_DICDI	YD25_MYCTU	Y278_MYCTU	K2C3_HUMAN	PER_DROSI	GRP1_ORYSA	LORI_MOUSE	MBN_DROME	GRP1_PHAVU	TBFG_EPTST	PER_DROPS
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400	603	957	629	959	165	481	196	252	603	1241
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159.5	159	159	158.5	158.5	157	157	156.5	155.5	155.5	155.5
34	9 9	37	38	36	40	41	42	43	44	45

ALIGNMENTS	RESULT 1 PHX5_MOUSE ID PHX5 MUSE STANDARD; PRT; 672 AA.	01-NOV-1998 (Rel. 08, Creat 01-NOV-1997 (Rel. 35, Last 15-JUN-2002 (Rel. 41, Last	Per-hexamer repeat protein PHXR5 OR PER.	Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost	-	RN [1] RP SEQUENCE FROM N.A.	MEDLINE=860143 Shin H.S., Bar	"An unusual coding sequence from a Drosophila clock gene i	Al IN VELCENTANCES.; Nature 317.445-448(1985). C craftabity. TO OPHED C.T. CREEDED COMPATING DECEMBETIC	000	This SWISS-PROT entry is copyright. It is produced through	between the Swiss institute of Bioinfo the European Bioinformatics Institute.	use by non-profit institutions as long as its content is in no	license agreement (or send an email to license@	BL; M12039; AAA88320.1;			; IPR00056 M00181; EG	124		Ouery Match 8.7%; Score 222; DB 1; Length 672; Best Local Similarity 41.7%; Pred. No. 6.4e-05; Matches 63; Conservative 16; Mismatches 46; Indels 26; Gaps 9;	Qy 360 GAGVEAVTVSVSATSNGTESGGAGSGTGTS-VSATSTLTGNG-GTESGGTA 408		×	Db 320 GTGTGTGTGTGTGTGTGTGSG-SGTGTGTGSGSGTAKVTGTATGTGT-GTDT 373	Qy 464 SSGTGAG-GAGSGGPSGHASNAKIPGIMTLT 493	Db 374 Gronglandings TAKVICIATIT 401
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A;Residues: 1-174 <LIW>
A;Cross-references: EMBL:X05806; NID:g11316; PIDN:CAA29249.1; PID:g1334349
C;Genetics:
A;Genome: chloroplast
C;Genetics:
C;Gen
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Search completed: July 16, 2003, 18:09:58 Job time: 61.3761 secs

Dβ	: 773 NDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGGSHSWEGEANKPKQ 832	Db 342 -KELTTEIDSNIEQMSSHKSEITELRRTVQGLEIELQSQLALKQSLE 387
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Qy Dp	471 GAGSGGPSGHASNA 484 	Oy 341 N-RDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGN 399 : : :
RESULT 13 KRME1 keratin, N.Alterna C.Species C.Date: 10 C.Accessi R.Krieg, J. Blol. A.Pitle: A.Referen A.Referen A.Recesiue A.Resiument C.Comment C.Comment C.Comment C.Comment C.Comment E.1144-457 F.1144-457 F.1144-457 F.1144-457 F.1144-457 F.114-1928 F.1191-1928 F.119	RESULT 13 KRWEI NATHERT 13 KRWEI NATHERT 13 KRWEI NATHERT 13 NATHERT 13	0y 400 GGTESGGTAGTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTSSEGAGSDKAGTGTS 459 1
Query Match Best Local Matches 11	y Match 7.5%; Score 192; DB 1; Length 569; Local Similarity 22.0%; Pred. No. 0.0053; hes 111; Conservative 68; Mismatches 192; Indels 134; Gaps 19;	QY 405 GGTAGTTTSSGTEAGGTSGTTTSSGAAGSGKAGTGTTGSEGAGSDKAGTGTSGT-TT 463
Qy Dp	19 GSLLA-SGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYAK 71	OY 464 SSGTGAGGAGSGCPSGHASNAKIPG 488
6	72 QFKSVVTTPADVAGYSDGFFIRGONLGAVGSVNEQPHTVGMSL 114	RESULT 15 800273 800273 800273 period clock protein - Acetabularia mediterranea chloroplast (fragment) C; Species: chloroplast Acetabularia mediterranea C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Jun-2000 C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Jun-2000 C; Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Jun-2000 R; Li-Weber, M.; de Groot, E.J.; Schweiger, H.G. Mol. Gen. Genet. 209, 1-7, 1987 A; Title: Sequence homology to the Drosophila per locus in higher plant nuclear DNA an A; Accession: S00273 A; Accession: S00273 A; Molecule type: DNA

Oy 471 GAGSGGPSGHASNA 484	SULT 12	period clock protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Species: Drov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999 C;Accession: A26588; S2942 R;Yu, Q.; Jacquier, A.C.; Citri, Y.; Hamblen, M.; Hall, J.C.; Rosbash, M. Proc. Natl. Acad. Sci. U.S.A. 84, 784-788, 1987 A;Title: Molecular mapping of point mutations in the period gene that stop or speed A;Reference number: A26588; MUID:8718249; PMID:3027703 A;Accession: A26588 A;Accession: A26588 A;Accession: A26588 A;Accession: A26588	A; Residence 1:1218 < YUQ> A; Residence: 1-1218 < YUQ> A; Residence: 1-1218 < YUQ> B; Kilman, R.M.; Hey, J. Genetics 133, 375-387, 1993 A; Title: DNA sequence variation at the period locus within and among species of the A; Reference number: S52935; MUD:93170641; PMID:8436278 A; Reference number: S52942 A; Status: preliminary; nucleic acid sequence not shown; translation not shown	A; Residues: 14-573 <kli> A; Residues: 14-573 <kli> A; Cross-references: EMBL:LO7818; NID:g158102; PIDN:AAA28776.1; PID:g552117 A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 19: A; Note: clone ME-NJ2 C; Genetics: A; Genetics:</kli></kli>	A;Cross-references: FlyBase:FBgn0003068 A;Introns: 32/2; 379/1; 498/1 C;Superfamily: period clock protein; EGF homology ·	Query Match Best Local S Matches 139	320 GLKSGGFGVIGRPVSYEPFRLGLTFREAPEEARPDNYM-VSNGTNMLLVICATPIKSSYK 3	9 IPADV AGVSDOFFIRGULGAVGSVER COMPANY GSVER COMPANY GSVER	439 TYETVMKKGQTAGASFCSKPYRFLIQNGCYVL-LETEWTSFVNPWSRKLEFVVGHH	494 RVFQGPKQCNVFEAAPTCKLKISEEAQSKNTRIKEDIVKRLAETVSRPS-238 YDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKA	: : :	597 PHHDYYDSKSSTETPPSYNQLNYNENLLRFFNSKPYTAPAELDPPKTEPPEPRGTCV		QY 378 ESG-GAGSGTGTSV-SATSTLTGNG-GTESGGTAGTTTSS	Oy 415 420
	Oy 471 GAGSGGPSCHASNA 484 : : : Db 893 GAGGGGAGAAAAA 906	RESULT 11 245427 period clock protein type A - fruit fly (Drosophila melanogaster) C; Species: Drosophila melanogaster C; Date: 19-Nov-1988 #sequence_revision 30-Jun-1991 #text_change 20-Aug-1999 C; Accession: A26427 R; Citri, Y.; Colot, H.V.; Jacquier, A.C.; Yu, Q.; Hall, J.C.; Baltimore, D.; Rosbash, M Nature 326, 42-47, 1987 Nature 326, 42-47, 1987 A; Title: A family of unusually spliced biologically active transcripts encoded by a Drose	A; Kererence number: A2642/; MUID:8/14460/; PMID:31029/0 A; Accession: A2642/; MUID:8/14460/; PMID:31029/0 A; Accession: A2642/; AUID:8/14460/; PMID:31029/0 A; Accession: A2642/; MUID:8/1460/; PMID:31029/0 A; Residues: 1-1218 <cit> A; Residues: 1-1218 <cit> A; Cross-references: GB:M30114; NID:g158056; PIDN:AAA28754.1; PID:g158059 A; Construction: A; Constructio</cit></cit>	%; 1005 12. 13	ESKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYAKOF 	79 TPADV-AGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNE :: :	QY 129 IYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN 185	OY 186 NMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG 237	QY 238 YDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKA 282	QY 283FDECKSNAIILKKKILDNDEDYKINFREMVNEVTCA 318 : : : :	OY 319 NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAV-TVSVSATSNGT 377 : :	'Qy 378 ESG-GAGSGTGTSV-SATSTLIGNG-GTESGGTAGTTTSS	QY 415 420 Db 773 NDEMEKFMLKKHRESRGRIGEKSKKSANDTLKMLEYSGPGHGIKRGGSHSWBGEANKPKO 832	421TSGTTTSGAASGKAG-TGTAGTTTSSEG-AGSDKAGTGTSGTTTSSGTGA-G	Db 833 QLTLGTDAIKGAAGSAGGAVGTGGVGSGGAGVAGGGGSGTGVAGTPEGRATTTSGTGTPG 892

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	QY 343 DVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGT 402 : : :
360 GAGVEAVIVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSG	OY 403 ESGCTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGT 458
416	QY 459 SGTTTSSGTGAGGAGSGGPSGHASNA 484 D
	RESULT 10 C26427 period clock protein type C – fruit fly (Drosophila melanogaster) C:Species: Drosophila melanogaster
666	C;Date: 19-Nov-1988 #sequence_revision 30-Jun-1991 #text_change 20-Aug-1999 C;Accession: C26A27 R:Citri, Y.; Colot, H.V.; Jacquier, A.C.; Yu, Q.; Hall, J.C.; Baltimore, D.; Rosbash, Nature 326, 42-47, 1987 A;Title: A family of unusually spliced biologically active transcripts encoded by a D A;Reference number: A26427; MUID:87144607; PMID:3102970 A;Accession: C26427
atin 10. Subd	A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-1176 <cit> A; Residues: 1-1176 <cit> C; Genetics: C; Genetics: A; Genetics: FlyBase: FBgn0003068 C; Genetics: Fright Partial Clock profesion: FGF homology</cit></cit>
A; Residues: 1-561 <zho> A;Cross-references: GB:J04029; NID:g623408; PIDN:AAA60544.1; PID:g623409 R;Korge, B-P; Gan, S.Q.; McBride, O.W.; Mischke, D.; Steinert, P.M. Proc. Natl. Acad. Sci. U.S.A. 89, 910-914, 1992</zho>	Ouery Match 7.7%; Score 196.5; DB 2; Length 1176; Best Local Similarity 22.6%; Pred. No. 0.0077; Matches 139; Conservative 65; Mismatches 229; Indels 181; Gaps 26;
A; Title: Extensive size polymorphism of the human keratin 10 chain resides in the C-term A; Reference number: A38182; MUID:92141228; PMID:1371013 A; Accession: A38182 A; Status: preliminary; not compared with conceptual translation	ISKEYEYEYHTELAKEHCKKEKCVNVDNIEDNNLKIYAKQFKSVVT 7
A; Mulecule Lype: UnNA A; Residues: 445-561 <kor> A; Note: sequence extracted from NCBI backbone (NCBIP:79433) C; Superfamily: cytoskeletal keratin C; Keywords: coiled coil</kor>	Qy 79 TPADV-AGVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNE 128 1
Query Match 7.7%; Score 197.5; DB 2; Length 561; Best Local Similarity 21.7%; Pred. No. 0.0026; Matches 110; Conservative 74; Mismatches 197; Indels 125; Gaps 20:	QY 129 IXHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN 185
18 DGSLLASGEVTSVISKEVEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYA 7 1 1 1 1 1 1 1 1 1	Qy 186 NMFQBALIRFRNASSEBMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG 237
1 2	Qy 238 YDFDYINTKKELVILASYLDGLDLIMERLIENFSDVNNTDDIKKA 282
GCEQIYNYEE 	Qy 2003FDECKSNAIILKKKILDNDEDYKINFREMVNEVTCA 318 : :
173 FIEKLRGARSEGNNMFQEALIRFRNASSEEWVNAASYLSAALFRYKEFDDE 1.	QY 319 NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAV-TVSVSATSNGT 377
LEKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAF 2 LTTELDNIRGISSYKSFITELRRNVOLEIELOSOLALKOSLEASL 3	Oy 378 ESG-GAGSGTGTSV-SATSTLTCNG-GTESGGTAGTTTSS
284 DECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFFRALNDLIISDCEKKGIKIN-R 3	Oy 415 420 DD 773 NDEMEKFWLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGGSHSWEGEANKPKQ 832
Db 387 AETEGRYCVQLSQIQAQISALEEQLQEIRAETECQNTEYQQLTDIKIRLE 436	TSGTTTSSGAASGKAG-TGTAGTTTSSEG-AGSDKAGTGTSGTTTSSGTGA-G

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A;Gene: Rv3512
C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homolo
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A;Residudes: 1-1079 <COL>
A;Cross-references: GB:ALO22022; GB:AL123456; NID:g3261554; PIDN:CAA17749.1; PID:g292
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holroyd,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Goi, Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holro Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete (A; Reference number: A70500; MUID:98295987; PMID:9634230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                273 LDGIISEVKAQYDS-----ICQRSKAEAETFYQSKYEEL--QITAGKHGDSVRNTKMEI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ------SNGTES 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       185 NNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDFDYIN 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 153 LDPFFENYISILRRKVDSLKSDQSRMESELKNMQDLVEEYRTKYEDEINKRTNAENEFVT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || :| | :| 325 SELNRMIQRLRSEIDGCKKQISQIQQNINDAEQRGEKALKDAQNKLNEIEDALSQCKEDC 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61; Mismatches 158; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 581;
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                                                                                                                                                                                                                                                                                                                                                                                              F;420-581/Domain: tail <END>
F;420-439/Region: H2 subdomain
F;440-581/Region: V2 and E2 subdomains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 20.3%
96; Conservative
                                     F)107-419/Domain: rod <ROD>
F)107-141/Region: coil 1A
F)142-153/Region: linker 1
F)154-254/Region: linker 12
F)255-271/Region: linker 12
F)272-290/Region: linker 2
F)291-298/Region: linker 2
F)291-298/Region: coil 2A
F)291-419/Region: coil 2B
F)357/Region: stutter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -ALNDLI--
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Best Local S.
Matches 96
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C;Species: Mus musculus (house mouse)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 20-Mar-1998
C;Accession: A02951
R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J. Biol. Chem. 260, 7142-7149, 1985
A;Tille: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Species: Hallotis rufescens (California red abalone)
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Accession: T08852
R; Shen, X.; Belcher, A.W.; Hansma, P.K.; Stucky, G.D.; Morse, D.E.
J. Biol. Chem. 272, 32472-32481, 1997
A; Title: Molecular cloning and characterization of lustrin A, a matrix protein from shell A; Reference number: 216496; MUID:98070424; PMID:9405458
A; Reference number: 216496; MUID:98070424; PMID:9405458
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNÅ
A; Residues: 1-1428 <SHE>
A; Cross-references: EMBL:AF023459; NID:92723361; PIDN:AAB95154.1; PID:92723362
A; Experimental source: tissue type mantle (shell and pearl nacre); cell type pallial
C; Superfamily: antileukoproteinase repeat homology
C; Keywords: extracellular matrix; extracellular protein
F; 1382-1426/Domain: antileukoproteinase repeat homology <ALP>
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                                                                                                                                                                373 TSNGTESGGAGSGT-GTSVSATST-LTGNGGTESGGT-AGTTTSSGTEAGGTSGTTTSSG 429
                                                                                                                                                                                                                                                                           AASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGT-----GAGGAGSGGPSGHAS 482
                                                                                                                                                                                                                                                                                                                                                     191 GGTGTGGTGTGTGTGTGT--GGTGTGGSGTGSGVEKLDAQGGTGGTAWDDGSDHDG 248
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Pred. No. 0.00
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lustrin A - California red abalone
Best Local Similarity 44.4%;
Matches 55; Conservative
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Residues: 1-581 <STE>
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Best Local
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geno

Db 523 AFGGSGGRGSSSGGCYSSGSSYGSGGRQSGSRGG-SGGGCSISGGGYGSGGGRY 579 Qy 433 GKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGGGPSGHASNA 484 Db 580 GSGG-GSKGGSISGGGKHSSGGGKHSSGGGSKGGSSGGGGSSSVKGSSGEAFGS 638 Qy 485 KI 486 Db 639 SV 640	A;Cross-references: GDB:118828; OMIM:148080 A;Map position: 17q12-17q21 A;Introns: 209/3; 237/2; 289/3; 343/3; 458/2; 592/3 A;Note: this gene encodes variants with considerable length polymorphism A;Note: this gene encodes variants with considerable length polymorphism A;Note: unttations in this gene can cause epidermolytic hyperkeratosis and keratosis p C;Complex: heterotetramer of two type I and two type II proteins, usually keratin 1 (C;Superfamily: cytoskeletal keratin C;Keywords: coiled coil; heterotetramer; intermediate filament; polymorphism F;1-145/Domain: head <hea> F;14456/Domain: helical rod *status predicted <rod> F;4456/Domain: tail <tal></tal></rod></hea>
RESULT 4 RESULT 10. RETAIL 10. type I, cytoskeletal - human N'Alternate names: cytokeratin 10	Query Match 8.4%; Score 216.5; DB 1; Length 593; Best Local Similarity 21.8%; Pred. No. 0.00028; Matches 111; Conservative 82; Mismatches 207; Indels 109; Gaps 19;
C;Specias: Indio Sapiens (man) C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 10-Dec-1999 C;Accession: S02158; C38182; B38182; PC1102; S14666; S14669 R;Rieger, M.; Franke, W.W.	Qy 18 DGSLLASGEVTSNFRYISKEYEFHTELAKEHCKKEKCVNVDNIEDNNLKIYA 70
J. Mol. Biol. 204, 841-856, 1988 J. M. Title: Identification of an orthologous mammalian cytokeratin gene. High degree of int A; Reference number: S02158; MUID:89125611; PMID:2464696 A; Accession: S02158 A; Molocula time Data	Qy 71 KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMS 113 ;
A.Residues: 1-593 <rie> A.Residues: 1-533 <rie> A.Cross-references: EMBL:X14487; NID:928316; PIDN:CAA32649.1; PID:928317 A.Experimental source: clone lambda-KH10-5</rie></rie>	QY 114 LEQFIKNELYSFSNEIYHTISS-QISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEE 172
R.Korge, B.P.; Gan, S.Q.; McBride, D.W.; Mischke, D.; Steinert, P.M. Proc. Natl. Acad. Sci. U.S.A. 89, 910-914, 1992 A.Title: Extensive size polymorphism of the human keratin 10 chain resides in the C-term A.Reference number: A38182; MUID:92141228; PMID:1371013	QY 173 FIEKLRGARSEGNNMEQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDEL 224
A.Accession: C.38184 A.Status: not compared with conceptual translation A.Molecule type: DNA A.Residues: 452-593 <kor1></kor1>	Qy 225 FKKANDNFGRDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFD 284 ::: : : : ::: Db 348 TTEIDNNFGAISSYKSEITERRNVALEIRLOSOLALKOSIEASLA 394
A;Cross-references: PIDN:AAB21315.1; PID:g244509 A;Mcte: sequence extracted from NCBI backbone (NCBIP:79427) A;Accession: B38182 A;Accession: preliminary; not compared with conceptual translation	285 ETEGRYCVQLSQIHAQISALEEQLQQIRAETECQNTEYQQLLDIKIRLEN
	QY 344 VISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNG 400
Gene 116, 245-251, 1992 A;Title: Exons I and VII of the gene (Kerl0) encoding human keratin 10 undergo structura A;Reference number: PC1102; MUID:92339897; PMID:1378806	QY 401 GTESGGTAGTTTSSGTAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAG 455
A:Molecule type: mRNA A:Molecule type: mRNA A:Residues: 'G',198-407,'Q',409-450,'G',452-486,491-524,534-593 <tka> A:Cross-references: GB:M77663; NID:g186628; PIDN:AAA59199.1; PID:g186629 A:Experimental source: embryonic skin, clone HK51</tka>	Qy 456 TGTSGTTTSGTGAGGAGSGGPSGHASNA 484 : :
<pre>K:Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M. Mol. Biol. Rep. 12, 277-283, 1987 A)Title: Sequence of a cDNA encoding human keratin No 10 selected according to structura A)Reference number: S14666; MUID:88122104; PMID:2448602 A)Accession: S14666</pre>	RESULT 5 T08080 probable myrosinase-binding protein - rape N.Alternate names: jasmonate inducible protein
A:Molecule type: mRNA A:Residues: 130-276,'YV',281-311,'I',313-339,'V',341-373,'R',375-407,'Q',409-459,'RS',46 56-579,'P',581-593 <dar1></dar1>	C;Species: Brassica napus (rape) C;Species: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000 C;Accession: T08080
A; Cross-references: EMBL:M19156; NID:g186769 A; Note: the sequence from Fig. 3 is inconsistent with the nucleotide sequence from Fig. 8; Darmon, M.Y.; Semat, A.; Darmon, M.C.; Vasseur, M. submitted to the EMBL Data Library, May 1988 A; Reference number: S14667	R;Geshi, N.; Brandt, A. Planta 204, 295-304, 1998 A;Title: Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L. s A;Reference number: 216340; MUID:98192006; PMID:9530873 A;Accession: T08080
A; Accession: \$14669 A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 130-278, 'YV', 281-311,'I',313-339,'V',341-373,'R',375-407,'Q',409-459,'RS',46 56-593 < ARRENGES: EMBL:M19156; NID:9186769; PIDN:AAA59468.1; PID:9307086 A; Note: the translated section of 10 Gentank party HIMMERTION release 111 0 Aiffore from	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-680 <ges> A;Cross-references: EMBL:Y11483; NID:e1023101; PIDN:CAA72271.1; PID:e304150 A;Experimental source: Cy Global; idolate a4; young seedlings</ges>
) 1 3 4 4 4 5	Query Match 8.4%; Score 216; DB 2; Length 680;

A:Note: translation of initiator Met is not shown R:Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R. I Biol Chem 260 7113-7118 1055	OY 319NTKFEALNDLI
A) Title: Amino and sequences of mouse and human epidermal type II keratins of M-r 67,00 (1) the filamont submits of m-r 67,00 (1) the filamont su	Db 389 SVRNSKIEISELNRVIQRLRSEIDNVKKQISNLQQSISDAEQRGENALKDAKNKLNDLED 448
e illament subunit eference number: A ccession: A02950	Oy 344VISSYKLLLSTITY-IVGAGVEAVTVSVSA 372
A; Molecule type: mRNA A; Residues: 151-183, 'K', 185-199,'M', 201-204,'K', 206-236,'S', 238-239,'R', 241-356,'Y', 358-	SH
	373 TSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSS-G
A; Experimental source: tissue neonatal foreskin A; Note: the authors translated the codon CUG for residue 476 as Met	Db 509 TSISGGGSRGGGGGGGSSYGSGGGSYGSGGGGGGGRGSYGSGGGSYGSGGSSYG 566
R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGiovanna, J.J.; Compton, J.G.; 9 Cell 70, 821-828, 1992	Qy 430 AASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSG 479
A:Title: A leucineproline mutation in the HI subdomain of keratin 1 causes epidermol A:Reference number: A43342; MUID:92386601; PMID:1381288	YGSGSSSGGYRGGSGGGGGSSGGR
A;Accession: A43342 Status: preliminary; not compared with conceptual translation	RESULT 3
A; Residues: 144-146, P', 148-159, 'P', 161-183, 'K', 185-186 <chi></chi>	
A;Cross references: GB:M90/0; GB:M11215; GB:M11845; GB:M11846; NID:g1843461 A;Note: sequence extracted from NCBI backbone (NCBIP:112784)	CK 2; epidermal cytokeratin 2
C:Comment: The cytoskeletal and microfibrillar keratins are classified into two types, that II Protein subunit appears to be a heterotetramer of two type I and two type II procedurate transfer of two type I and two type II procedurate transfer of two type II procedurates the contract of the contract o	n 31-Dec-1993
C.Comments. Notatin 1 is expressed in community differentialing epidemins. 3. Actor (CDB. FDB.)	o., Odnayodni, O.F., Franke, m
A.Cross-references: GDB:128198; OMIM:139350	1 Cyconstanti 2, am epideimai Cycosneiecai pioteim 32380238; PMID:1380918
position: 12q11-12q13 e: defects in this gene may result in epidermolytic hyperkeratosis	Accession: A4486 Molecule type: m
C:Complex: heterotetramer of two type I, usually keratin 10 (see PIR:KRHU0), and two typ C:Superfamily: cytoskeletal keratin	Residues: 1- Cross-refere
<pre>C.Keywords: coiled coil; heterotetramer; intermediate filament F.4-179/Domain: head <hed></hed></pre>	imental source: epidermis the authors translated the codon GGC f
F;4-143/Region: El and VI subdomains F;14-179/Region: H1 subdomain	sequence extracted from NCBI backbone (NCBIN:112351)
F;180-492/Domain: rod <rod></rod>	ı H
-226/Region: linke	8.5%; Score
-34/Region: linke	Similarity 22.1%; Fred. NO. 0; Conservative 100; Mismat
371/Region:	Qy 11 GIHYYXIDGSLLASGEVTSNFRYISKEYEHTELAKEHCKKEKCVNVDNI 61
ion: stutter	Db 155 GIHEVSVNQSLLQPLNVKVDPEIQNVKAQEREQIKTLNNKFASFIDKVRFL 205
-512/Region: H2	Qy 62 EDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVG 111
·643/Region: V2 and E2 subd	206 EQONOVLOTRWELLQQMNVGTRPINLEPIFQGYIDSL
tch 8.6%;	ANALYUYYUYAAAAA ANAAAAA KUUNTA KUUNTA AUUNTA AYUYAMIIIA WAXGAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
Best Local Similarity 23.0%; Fred. No. 0.00021; Matches 125; Conservative 76; Mismatches 152; Indels 177; Gaps 28;	IIZ MSLEQFIKNELYSFSNELYHTISSQLSNSFELMMSDALVKHUN-YLLAKKEGEGCEQINN :: ::: :: :: :: : : : : : :: : :: : :
OV 85 GVSDGFFIRGONIGAVGSVNEODNTVGMSLEOFIKNEIVSFSNEIV 130	Db 263MQDLVEDYKKKYEDEINKRTAAENDFVTLKKDVDNAYMIKVELQSKVDLLNQ 314
126 GFGGGGGGGGGGGGGGTGCTQFT.TINQSLLQPLNVEIDPEIQKVKSREREQI	171 E-EFIEKLRGARSEGNNMFQEALIRFRNASSEEMVNAASYLSA
	Db 315 EIEFLKVLYDAEISQIHQSVTDTNVILSMDNSRNLDLDSIIAEVKAQYEEIAQRSKEEAE 374
184 OSLNNOFA-SFIDKVRFLEGONOVLOTKWELLOOVDTSTRTHNLEEVEESFINNLRRG	QY 213 ALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSD 272
181RGECNNMEOPELIBERNA SCREMMINA & CVI CA A LEDVERENDEL BEKKAN	Db 375 ALYHSKYEELQVTVGRHGDSLKEIKIEISELNRVIQRLQGEIAH 418
241 VDOLKSDOSRLDSELKNM-ODMVEDYRNKYEDEINKRYN	Qy 273 VNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALND 327
NVADENET TERMINATION OF THE PROPERTY OF THE PR	NVQDAIADAEQRGEHALKDARN
279AENEFVIKKDVDGAYMTKVDLQAKLDNLQQEIDFLTALYQAELSQMQTQIS	328LIISDCEKKGIKINRDV-ISSYKLLLSTITYIVGAGVEAVTVSVSA
QY 275 NTDDIKKAFDECKS-NAIILKKKILDNDEDYKINFREMVNEVTCA 318	463 ARLLRDYQELMNVKLALDVEIATYRKLLEGEECRMSGDLSSNVTVSVTSSTISSNVASKA
HGD	Qy 373 TSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAAS 432
•	

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 16, 2003, 17:50:14 ; Search time 59.3761 Seconds Run on:

(without alignments)
814.396 Million cell updates/sec

US-09-853-079-52 Perfect score:

2565 1 KRENEHTDMNGIHYYYIDGS.....AKIPGIMTLTLFALLTFIVN 503 Sednence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters:

283224 segs, 96134422 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	period clock prote	keratin 1, type II	keratin, 67K type	$\overline{}$	probable myrosinas	lustrin A - Califo	keratin, type II c	hypothetical glyci		period clock prote		clock		variant surface an	period clock prote	. keratin, epidermal	circadian rhythm p	hypothetical glyci	hypothetical glyci			hypothetical glyci	10	hypothetical glyci		hyphally requlated	endo-1,4-beta-gluc	hypothetical glyci	
SUMMARIES	ΩΙ	UMMS	KRHU2	A44861	KRHUO	108080	T08852 .	KRMS2	B70807	A31994	C26427	A26427	A26588	KRMSE1	S18654	S00273	S07330	A25018	D70807	F70806	S66852	F70963	E70806	A43855	A70934	T28125	S58135	E82759	C70974	B70893
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æ	Query	8.7	8.6	8.5	8.4	8.4	7.8	7.8	7.7	•	7.7	7.7	7.7	7.5	7.4	7.3	7.3	7.3	7.3		7.2	•	7.2	7.1	7.1	7.0	7.0	6.9		
	Score	222	219.5	217	216.5	216	200.5	199	198	197.5	196.5	196.5	196.5	192	190.5	188.5	188.5	186	186	185	184	183.5	183.5	182.5	181	180	178.5	178	177	176
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hypothetical glyci	nuclear antigen EB	hypothetical prote	period clock prote	hypothetical glyci	hypothetical prote	keratin, 54K type	hypothetical glyci	glycine-rich prote	keratin, 70k type	period clock prote	1,4-beta-cellobios	sericin1B - silkwo	hypothetical prote	secreted acid phos	hypothetical glycl	
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176	176	176	175.5	175.5	175	174	174	173.5	173	173	173	173	172.5	172	171.5	
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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RESULT 1
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period clock protein - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000

Accession: A24403
R.Shin, H.S.; Bargiello, T.A.; Clark, B.T.; Jackson, F.R.; Young, M.W.
Nature 317, 445-448, 1985
A.Title: An unusual coding sequence from a Drosophila clock gene is conserved in vert A; Reference number: A24403; MUD:86014384; PMID:2413365
A.Accession: A24403
A.Accession: A24403
A.Molecule type: DNA
A.Residues: 1-713 <SHI>
A.Residues: 1-713 <SHI>
A.Comment: Mutations within the per locus of the fruit fly affect a variety of natura logus locus with multiple tandem repeats of nucleic acid hexamers (ACNGGN, TCAGGC) t C; Comment: Mte serine residues of the SG repeats found in certain proteoglycans are C; Superfamily: period clock protein; EGF homology
C.Keywords: circadian rhythm; tandem repeat

9 26; Gaps 8.7%; Score 222; DB 1; Length 713; 41.7%; Pred. No. 0.00018; Live 16; Mismatches 46; Indels ; 63; Conservative Similarity Query Match Best Local S Matches 63

360 GAGVEAVTVSVSATSNGTESG-----GAGSGTGTS-VSATSTLTGNG-GTESGGTA 408 ö g

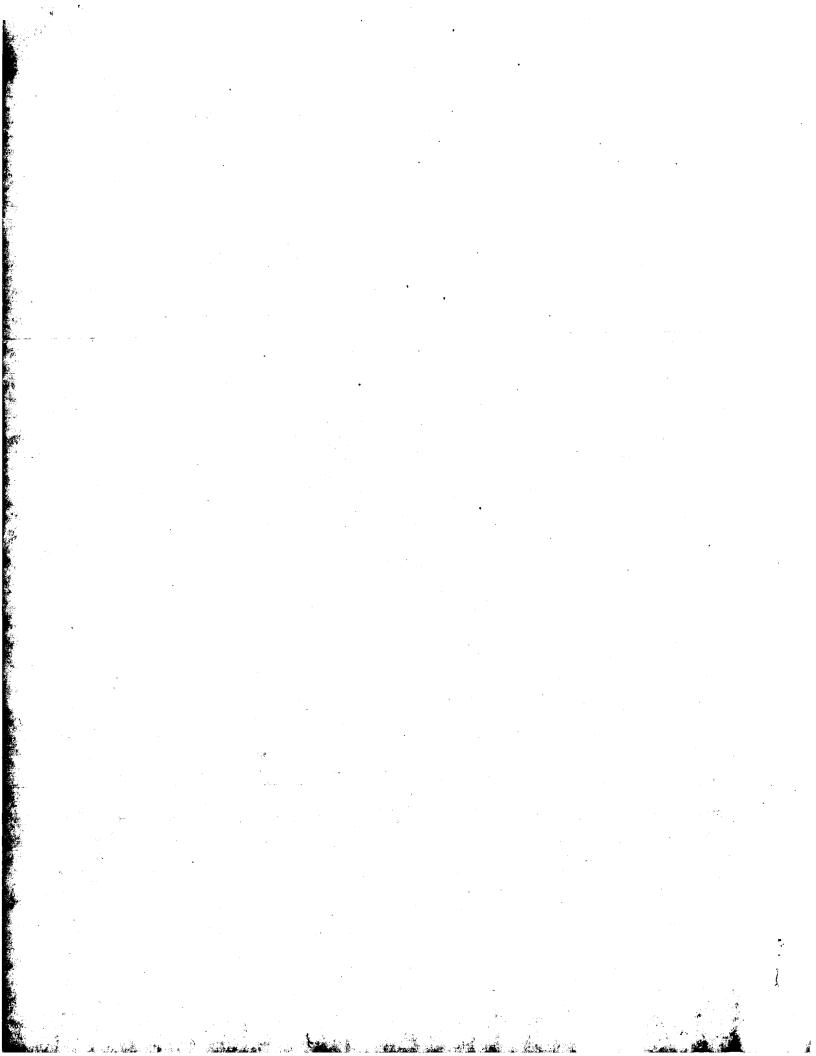
409 GTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK-----AGTGTSGTTT 463 ò

g Qγ

464 SSGTGAG-GAGSGGPSGHASNAKIPGIMTLT 493

qq

National I, type II, cytoskeletal - human
NiAlternate names: 67K type II epidermal keratin; cytokeratin I
C; Species: Homo sapiens (man)
C; Date: 04-Dec-1986 #sequence_revision 22-Oct-1999 #text_change IO-Dec-1999
C; Accession: A22940; A02950; A43342
K; Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985
A; Reference number: A22940; MUID:85166239; PMID:2580302
A; Accession: A22940
A; Molecule type: DNA
A; Residues: 1-643 < JOH>
A; Cross-references: GB:M98776; GB:M1215; GB:M1845; GB:M11846; NID:g1843461



138 SNSFLIMMSDAIVKHDNYILKKEGEGCEGIYNYEEFIEKLRCAR 181 13.2 CLSYIYKHSVMILERDRYNDGHKDYIEEKTKEKNKLKKELEKCFPEGY 179 18.2 SECNNMFOGALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240 18.1	301 DEDYKINFREMVNEVTCANTKFFALNDLIISDCEKKGIKINRDVISSYKLLLSTITYI 358	SULT 15 Sequence 49, Application US/09853079 Sequence 49, Application US/09853079 Publication No. US2030109689A1 Sequence 49, Application US/09853079 Publication No. US2030109689A1 APPLICANT: Lodes, Michael J. APPLICANT: Houghton, Raymond L. APPLICANT: Sleath, Paul R. APPLICANT: Sleath, Paul R. APPLICANT: Scrist, Heather TITLE OF INVENTION: COMPOUNS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNS AND TREATMENT OF B. MICROII INFECTION TITLE OF INVENTION: AND TREATMENT OF B. MICROII INFECTION FILE REFERENCE: 210121.426C11 CURRENT APPLICATION NUMBER: US/09/853,079 CURRENT FILING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 224 SOUTHARE: FastSEQ for Windows Version 3.0 LENGTH: 367 TYPE: PRT TYPE:	Similarity 2; Conserv PADVAGVSD- :: : : PSEAGGPSEA SNSFLIMMSD :: -: + CLSTITKHSV SEGNNMFQEA SIGNNMFQEA DYINTKKEE DYINTKKEE + DEDYKINFRE DEDYKINFRE DEDYKINFRE DEDYKINFRE
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342 ITKVSNVIIPGIKALTLTV 360

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Search completed: July 16, 2003, 18:08:38 Job time: 84.2782 secs

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Reed, Steven G.
Lodes, Michael J.
Houghton, Raymond
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Best Local Similarity
                                                                                                                                                                                                                                                        ; ORGANISM: Babesia
US-09-737-178-144
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US-09-286-488-49
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                                                                                                           Gaps
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Bloughton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
APPLICANT: Moner, Mary
APPLICANT: Gerrist, Heather
TITLE OF INVENTION: AND TREATMENT OF B. MICROI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
                                        Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44.5%; Score 1141; DB 9; Length 677; 100.0%; Pred. No. 2.5e-65; Live 0; Mismatches 0; Indels (
                                                                   Indels
                                       Score 1143; DB 10;
Pred. No. 1.8e-65;
2; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 144
LENGTH: 677
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US-09-737-178-144
; Sequence 144, Application US/09737178
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Publication No. US20030109689A1
GENERAL INFORMATION:
                                        44.6%;
99.1%;
                                       Query Match
Best Local Similarity 99.13
Matches 228; Conservative
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US-09-853-079-144
; ORGANISM: Babesia
US-09-737-178-85
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US-09-853-079-144
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Best Local S
Matches 228
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276 TDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEK 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAG 455
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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R:
APPLICANT: Sleath, Paul R:
APPLICANT: Sleath, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210.11.426CJ
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       456 TGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
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                                                            APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000.12-13
NUMBER OF SEQ ID NOS: 144
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Pred. No. 2.5e-65;
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28.8%; Pred. No. 2.5e-08;
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100.0%; Pred. No. ...
0; Mismatches
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Sequence 49, Application US/09286488

Setent No. US/0020169136A1

GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
ij
                      Sleath, Paul R.
McNeill, Patricia D.
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Oy 447 EGAGSDKAGTGTSGTTTSSGTGAGGGGGPSGHASNAKIPGIMTLTLFALLTFIVN 503 1	APPLICANT: Homer, Mary APPLICANT: Becrist, Heather TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION FILE REFERENCE: 210121.426C11 CURRENT APPLICATION UNDER: US/09/853,079 CURRENT FILING DATE: 2204 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 85 LENGTH: 666 TYPE: PRT TYPE: PRT ORCANISM: Babesia	Query Match 44.6%; Score 1143; DB 9; Length 666; Best Local Similarity 99.1%; Pred. No. 1.8e-65; Indels 0; Gaps 0; Matches 228; Conservative 2; Mismatches 0; Indels 0; Gaps 0; Qy 274 NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREWVNEVTCANTKFEALNDLIISDC 333 Db 7 HHTDDIKKAFDECKSNAIILKKKILLDNDEDYKINFREWNDEVTCANTKFEALNDLIISDC 66	QY 334 EKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSAT 393	OY 454 AGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503	; Sequence 85, Application US/09737178 ; Patent No. US20010029295A1 ; GENERAL INFORMATION: APPLICANT: Rede, Steven G. APPLICANT: Lodes, Michael J. APPLICANT: Houghton, Raymond L. APPLICANT: Sleath, Paul R. APPLICANT: Houghton, Paul R. APPLICANT: Houghton, Paul R. APPLICANT: Homer, Mary	APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION CURRENT APPLICATION NUMBER: US/09/737,178 CURRENT FILING DATE: 2000-12-13 NUMBER OF SEQ ID NOS: 144 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 85 LENGTH: 666 TYPE: PRT
11	RESULT 9 US-09-737-178-87 Sequence 87, Application US/09737178 Patent No. US20010029295A1 Fatent No. US200100029295A1 GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Lodes, Michael J. APPLICANT: Houghton, Raymond L. APPLICANT: Aleath, Paul R. APPLICANT: MCNeill, Patricia D. APPLICANT: Homer, Mary APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS	TILLE OF IN FILE REFEREN CURRENT APPI CURRENT FILI NUMBER OF SE SOFTWARE: E SEQ ID NO 87 LENGTH: 113 TYPE: PRT	ORGANISM: Babesia -09-737-178-87 Query Match 45.2%; Score 1159.5; DB 10; Length 1132; Best Local Similarity 58.3%; Pred. No. 3e-66; Matches 278; Conservative 35; Mismatches 89; Indels 75; Gaps	59 DNIEDNNLKIYA-KREKSVYTTPADVAGVSDGFFIRGONGAVGSVNEQPNTVGM	OY 1/2EFIERLEGARGEGINMFQEALIFFRNASSEEMVNAASYLSAALFFKKE 219 Db 369 IDFSKREATDSGSFTDILLGNKVKESLSFIEGLISDIKSHSLKAGVTGGISSSSLF 424 OY 220 FDDELFKRANDNFGRDGYDFDYINTKKELVILASVLDGLDLIMERL 266 Db 425DELFKANDNFGRDGYDFDYINTKKELVILASVLDGLDLIMERL 266 Db 425DELFKANDNFGRDG	

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DNI-----EDNNLKIYA-KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM 112
                                                                                                                                                                                                                                      269 DNITTTRNEVTKDDVYALKKALTCLTTHLIYHSKVDG--ISFDMLGTQKNKSSPLGKIGT 326
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                                                     ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
                                                                                                                                                                      RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
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 73 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN 132
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROIL INFECTION
FILE REFERENCE: 210121.426C11
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58.3%; Pred. No. 3e-66;
ive 35; Mismatches 89; Indels
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 87, Application US/09853079; Publication No. US20030109689A1; GENERAL INFORMATION:
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278; Conservative
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US-09-853-079-87
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Balth, Parlicia D.
APPLICANT: Momer, Mary
APPLICANT: Heather
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42669
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT APPLICATION NUMBER: US/09/737,178
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 6.9e-129;
); Mismatches 2;
                                   Windows Version 3.0
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 2001-05-09
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99.5%;
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99.5%;
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Best Local Similarity 99.5%
Matches 417; Conservative
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Best Local Similarity 99.5
Matches 417; Conservative
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                                                                                                   ORGANISM: Babesia microti
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
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                                                                                                                                                                  APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Paul R.
APPLICANT: Moner, Mary
APPLICANT: Honer, Mary
APPLICANT: Honer, Mary
APPLICANT: Gecrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121-42671
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOGTWARE: FastSEQ for Windows Version 3.0
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89.0%; Pred. No. 5.9e-136;
ive 0; Mismatches 4;
                                                       ASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                 Sequence 209, Application US/09853079
Publication No. US20030109689A1
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US-09-853-079-209
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                                                                                                        RESULT 4
US-09-853-079-209
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                                                                                GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: McMeill, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C3
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEO ID NOS: 83
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REPERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
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Pred. No. 6.9e-129;
0; Mismatches 2;
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Moneill, Patricia D.
APPLICANT: Homer, Mary
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99.5%;
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US-09-286-488-21
                                             Sequence 21, Application USPatent No. US20020169136A1
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RESULT 5
US-09-286-488-21
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DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Moneill, Patricia D.
APPLICANT: Moneil, Patricia D.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121,42669
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
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SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20010029295A1
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CORGANISM: Babesia microti
US-09-737-178-52
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Matches 503; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 52, Application US/09853079 Publication No. US20030109689A1 GENERAL INFORMATION:
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APPLICANT: Reed, Steven G.
APPLICANT: LOGGE, Michael J.
APPLICANT: Lodge, Michael J.
APPLICANT: Lodge, Michael J.
APPLICANT: General J.
APPLICANT: General J.
APPLICANT: General J.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
CURRENT FILING DATE: 1999-04-05
CURRENT FILING DATE: 1999-04-05
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 52
LENGTH: 503
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Pred. No. 9.3e-157;
Mismatches 0;
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US-10-123-155-3

US-10-146-731-3
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US-09-286-488-24
US-09-833-079-24
US-10-184-644-107
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US-10-184-644-207
US-10-184-644-207
US-10-184-634-207
US-10-123-155-155
US-10-123-155-155
US-10-123-155-433
US-10-123-155-433
US-10-146-731-433
US-10-184-644-417
US-10-184-644-417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-737-178-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    451899 segs, 118759770 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Match ]
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2565 2565 2239.56 2239.5 2130 2130 2130 2130 2140.5 1141 1141 1141 1141 1141 246.5 246.5 239.5 239.5

Score

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Result

Gaps

914 AA; 100583 MW; 7E7A9B3A5BAA53C2 CRC64;

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SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FL131022 fis, clone NT2RP3000753, weakly similar to neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNa sequencing project."; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AR000361; BAA91111.1; -
EMBL; SM00049; DEP:
SMART; SM00049; DEP:
SMART; SM00049; DEP:
11.
                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Wasaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Shishikawa T., Nagai K., Suqano S., Ishibashi T., Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoka S., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                               Score 36; DB 11; Length 465;
Pred. No. 34;
4; Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 692;
52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14; Indels
to the EMBL/GenBank/DDBJ databases.
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"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023084; BAB14396.1;
                                           EMBL; AF290205; AAL27891.1; JOINED.
EMBL; AF290206; AAL27891.1; JOINED.
EMBL; AF290207; AAL27891.1; JOINED.
SEQUENCE 465 AA; 49160 WW; 52A263D653DA8F80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         692 AA; 79146 MW; 9B6101C81EFC8564 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            914 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           692 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                              23 NGNETSTSAIKSSTVQSHQSATTSTE 48
                                                                                                                                                                                                                                                                  6 NXNKSXXAXXKSXDTQTXQEXXXXXE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     470 HSEENIQKPFSAGFKRTSTLTVQD 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 HXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA FLJ20354 fis, clone HEP15013.
Homo sapiens (Human).
                                                                                                                                                                                                                    4,
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                                                                                                                                                                  33.3%;
26.9%;
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nes 8; Conservative
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9H945;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                  Bap-like protein Bhp.
Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
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41.2%; Pred. No. 1.9e+02;
.ive 2; Mismatches 8; Indels
                      Length 914;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TIGREAMS; TIGROLIG7; LPXTG_anchor; 1.
TIGREAMS; TIGROLIG8; YSIRK_signal; 1.
PROSITE; PSSO144; FILANIN_REPEAT; 2.
PROSITE; PSSO343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 2402 AA; 258095 WW; D5807D96B8FZE9CC CRC64;
                                                                  8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY028618; AAK29746.1; -InterPro; IPR001298; Filamin. InterPro; IPR001899; Gram.pos_anchor. InterPro; IPR003410; Hyalin.
                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                    Score 36; DB 4;
Pred. No. 69;
2; Mismatches 6
                                                                                                                                                                                                                                                           PRT; 2402 AA.
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                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00746; Gram_pos_anchor; 1. Pfam; PF02494; HYR; 1. Pfam; PF00801; PKD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000601; PKD_domain.
                                                                                                        4 KXNXNKSXXAXXKSXDTQ 21
                                                                                                                                     125 KSADTQTTNETTNKNDD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 KSXDTQTXQEXXXXEE 32
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Ol-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41.2%;
                                            44.48;
Query Match
Best Local Similarity 44.*.,
Best Local 8; Conservative
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Best Local Similarity 41.2.
Local 7; Conservative
                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biofilm Formation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Staphylococcus
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RA Adams M.D., Celnither S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celnither S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celnither S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celnither S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA George R.A. Lewis S.E., Fitchards S., Asbhurner M., Henderson S.N.,
RA Button G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Man K.H., Doyle C., Baxer E.G., Hald G., Chandre D., Beliffer B.D.,
RA Ballew R.M., Basul A., An H.-J., Andrews-Fennkoch C., Baldwin D.,
RA Ballew R.M., Basul A., Berman B.P., Bhandari D., Belshakov S.,
RA Butts K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,
RA Butts K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,
RA Butts K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,
RA Candry J.M., Cawley S., Dahlke C., Davaneport L.B., Davies P.,
RA Butts K.C., Busam D.A., Buttler H., Cadieu E., Center A., Chandra I.,
RA Cong F., Gorrell J.H., Guz C., Ferraz C., Ferraz C., Ferraz C.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Pluck J.,
RA Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Ketchum K.A.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Methor B.E., Kodira C.D., Merrik C., Mraytz S., Wulp D., Lai Z.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.R.,
Randert K., Remington K.A., Mixon K., Musskerin D.R., Paceb J.M.,
Ralaszolo M., Pittman G.S., Pan S., Pollard J., Wang X.,
Randert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Stuong R., Sun E.,
Randry Z.-Y., Wostage T.W., Woldey W., Wolder W., Wold M., Rullams S.M., Woodage T., Worley K.C., Wu Supskeri M.P., Wang R.Y.,
Randry Z.-Y., Wassariman D.A., Wallston C.B., Shub S., Zhoo O., Zhoo O. Shub R., Shong S., Zhon M., Zhong S., Zhon O., Zhon S., Zh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36; DB 5; Length 400;
Pred. No. 29;
3; Mismatches 19; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              317 HEFPNRNEEDQATRRSESTSTQAETGPQTQE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 HXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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   MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FlyBase; FBgn0039267; CG13649.
InterPro; IPR003889; FYrich_C.
InterPro; IPR003888; FYrich_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33.3%;
29.0%;
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Best Local Similarity 29.00
Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Podocalyxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00542; FYRC;
SMART; SM00541; FYRN;
SEQUENCE 400 AA; 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SVJ;
Kershaw D.B., Li J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08VI04;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8VIQ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PODXL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota, Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13; Indels
                   Verhasselt P., Volckaert G.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; X89514; CAA61704.1; -.

EMBL; X71258; CAA62637.1; -.

EMBL; Z73289; CAA97695.1; -.

EMBL; U53877; AAB82372.1; -.
                                                                                                    Delius H.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                    SEQUENCE FROM N.A.
Dellus H., Hebling U.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wilson R., Waterston R.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                           Pauley A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                          Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S0004116; YLR126C.
rPro; IPR000991; GATase_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 32.03
Matches 8; Conservative
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STRAIN=FY23 /RD005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [1]
SEQUENCE FROM N.A.
STRAIN-BERKELEY;
                                                                   SEQUENCE FROM N.A. STRAIN=S288C;
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-S288C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9VBY9
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PRELIMINARY;
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                                                                                                                                                  Query Match
Best Local Similarity
7; Conserve
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9; Conserva
                                                                                                                                       608 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-BERKELEY;
                        STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORF YLR126C
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                                                                                                                                       SEQUENCE
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STRAINEL TOR NI6961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana (Mouse-ear cress).

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=COLUMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 16; Length 290;
13;
 Length 241;
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                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 AA; 32611 MW; 2E3CC4062C2055E5 CRC64;
                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 3, BAC clone: T19N8.
                        13;
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DB :
Score 37; DB:
Pred. No. 11;
1; Mismatches
                                                                                                                            290 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 13;
                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotat:
Pseudouridine synthase family 1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00849; Pseudou_synth_2; 1.
TIGRFAMs; TIGR00093; Cons_hypoth93; 1.
PROSITE; PS01149; PSI_RSU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR004197; Cons_hypoth93.
InterPro; IPR000613; PseudoU_synth.
InterPro; IPR000748; Psi_RSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHPPTRANRKSVANKKKNATQT 100
                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GHXKXNXNKSXXAXXKSXDTQT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                  GHPPTRANRKSVANKKKNATOT 51
                                            1 GHXKXNXNKSXXAXXKSXDTQT
                                                                                                                                                                                                                                                                                                                                                                                              Nature 406:477-483(2000).
EMBL; AE004194; AAF94299.1; -.
34.38;
36.48;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8; Conservative
                       Conservative
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                                                                                                                           PRELIMINARY;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sest Local Similarity
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                                                                                                                                                                                                           Vibrio cholerae.
                                                                                                                                                                                                                                NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                      TIGR; VC1140;
                                                                                                                                                                                                                                                                                                                                                              Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                     cholerae.
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                                                                                                                                       O9KSW6
                                                                                                                           Q9KSW6
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                       Matches
                                                                                                    RESULT 7
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Q9LH95
                                                                                                                O9KSW6
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Nakamura Y.;
Nakamura Y.;
Nakamura Y.;
Nakamura Y.;
Squence features of the regions of 4,251,695 bp covered by ninety Pl,
TAC and BAC clones.';
DNA Res. 7:217-221(2000).
EMBL; AP002057; BAB03177:1;
InterPro; IPR02965; P_rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                           Length 608;
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                                                                                                                                                                                                                                                                                                                                                                                   13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY071126; AAL48748.1; -SEQUENCE 198 AA; 22012 MW; CE33F831FAB79D49 CRC64
                                                                                                                                                                                                                                                                62766 MW; 6C6368AF4BD2A3B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                        Score 37; DB 10;
Pred. No. 28;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 HXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.3%; Score 36; DB 29.0%; Pred. No. 14; iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                        34.3%; Score 37; 29.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YLR126C OR L3105 OR L3101 OR L9233.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  429 NSKSSSSSSTTSVKEVETQTSSE 452
                                                                                                                                                                                                                                                                                                                                                                                                                                             2 HXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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MEDLINE=20363099; PubMed=10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21,
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DOMAIN
SEQUENCE
                                                                    subtilis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., SEQUENCE OF 27-37 AND CHARACTERIZATION.
MEDIINE-99140137; Pubmed=10206711;
Margot P., Pagni M., Karamata D.;
"Bacillus subtilis 168 gene lytF encodes a gamma-D-glutamate-meso-diaminoplmelate muropeptidase expressed by the alternative vegetative
                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                   ij
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Endopeptidase LYTF precursor (Cell wall-associated polypeptide
CWBP49).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                    Length 1033;
                                                                                                                                                                                                                                                 11; Indels
                                                                                                                                                                                    1033 AA; 114266 MW; 559659540BDE66F5 CRC64;
                                                                                                                                                ATP-binding; Immunoglobulin domain; Transferase;
Tyrosine-protein kinase.
SEQUENCE 1033 AA; 114266 WW; 559659540BDE66F
                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                488 AA.
                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                   Score 38.5;
Pred. No. 24
                                                                SMART; SM00408; IGC2; 3.
SMART; SM00410; IG_1ike; 2.
SMART; SM00219; TYPKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                        1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98044033; PubMed=9384377;
                                                 PD000001; Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sigma factor, sigma-D.";
Microbiology 145:57-65(1999).
                                                                                                                                                                                                                   35.6%;
40.0%;
                                PRINTS; PR00109; TYRKINASE
Pfam; PF00047; ig; 5.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                  Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                   Query Match
                                                   ProDom;
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Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBl_TaxID=666;
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Pred. No. 14;
                                                                                                                                                                                       Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF261151; AAG16128.1; ..
InterPro; IPR004397; Cons_hypoth93.
InterPro; IPR006613; Pseudod_synth.
InterPro; IPR006748; Psi_RSU.
InterPro; IPR00991; Psi_RSU.
IIGRFAMS; TIGR00093; Cons_hypoth93; 1.
PROSITE; PSO1149; PSI_RSU; 1.
SEQUENCE 241 AA; 26964 MW; F12D39E90911079F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Signal; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6FE0E96A4B42BDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pseudouridylate synthase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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POLY-THR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 KXNXNKSXXAXXKSXDTQT 22
                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C40.002; -. InterPro; IPR002482; LysM. InterPro; IPR00064; NLPC_P60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51397 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.2%;
36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF01476; Lysm; 5.
Pfam; PF00877; NLPC_P60; 1.
SMART; SM00257; Lysm; 5.
Cell wall; Hydrolase; Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 30...
7; Conservative
                                                                                                     Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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488
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163
172
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288
305
355
488 AA;
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OTK protein.
OTK OR CG8967.
  Query Match
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09v643;
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                                                                                                                         Lodes M.J., Houghton R.L., Brinsma E.S., Mohamath R., Reynolds L.D., Benson D.R., Krause P.J., Reed S.G., Persing D.H.; "Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                          Babesia microti.
Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pulido D., Campuzano S., Koda T., Modolell J., Barbacid M.;
"Dtfk, a Drosophila gene related to the trk family of neurotrophin
receptors, encodes a novel class of neural cell adhesion molecule.";
EMBO J. 11:391-404(1992).
                                                                                                                                                                                                                                                                                                               0
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SMART; SM00410; IGC2; 3.
SMART; SM00219; TYRC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Cell adhesion; Immunoglobulin domain; Signal;
                                                                                                                                                                                                                                                                                  Length 275;
                                                                                                                                                                                                                                                                                                                14; Indels
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W; D282EFCB28ACA8D0 CRC64;
                                                                                                                                                                                                                                        275
30775 MW; C3CC5D5EBC494E01 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last annotation update) Seroreactive antigen BMN1-20 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                73.1%; Score 79; DB 5; I 56.2%; Pred. No. 2.4e-08; tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                         1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1033 AA
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                                                                                                                                                                                                                            POTENTIAL.
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InterPro; IPR000719; Buk_pkinase.
InterPro; IPR000719; Buk_pkinase.
InterPro; IPR0013698; Ig_2.2.
InterPro; IPR0013609; Ig_like.
InterPro; IPR001445; Tyr_pkinase.
Pfam; PP00047; Ig; 5.
Pfam; PP00067; Ig; 5.
ProDom; PD000001; Euk_pkinase; 1.
                                                                                              STRAIN=MN1;
MEDLINE=20231818; PubMed=10768973;
                                                                                                                                                                               Infect. Immun. 68:2783-2790(2000).
EMBL; AF206527; AAF68255.1; -.
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STRAIN-CANTON S;
MEDLINE-92164624; PubMed-1371458;
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                                                                                                                                                                                                                                                                                                Local Similarity 56.2 es 18; Conservative
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OTK OR DTRK OR CG8967
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275
275 AA;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
                                                        NCBI_TaxID=5868;
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                                                                                                                                                                     Babesia microti.
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SEQUENCE
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortuna J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Button G.G., Wortuna J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Abril J.E., Agbayan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Basus D.W., Barman B.P., Bhandari D., Bolshakov S.,
RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Guan P., Harris M.,
RAISSH F., Ratpen G.H., Ke Z., Kannison J.A., Recthum R.A.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodire C.D., Kraft C., Kratt E., Kolre C.D., Kraft C., Kratt C., Kratt C., Kratt E., Morne S.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M. Wurphy B., Murphy L., Murny D.M., Nelson D.L.,
Rabison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J. M.,
Siden K.M., Woy M., Wurphy B., Murphy L., Wurny D.M., Nelson D.K.,
Nelson D.R., Wassarman D.A., Walshaw S., Wang S., Yao Q.A.,
Rabisara R., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Woodage T., Stangson M., Strong R., Sun E.,
Rand Z., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhon R.,
Rander R., Shore S., Worley S., Whyers E.W., Rolling M., Zhong S., Zhon R.,
Rander R., Shore S., Worley S., Roll D., Sarong S., Sanith H.,
Rander R., Shore S., Ro
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                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Length 1033;
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                       11;
       DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1033 AA.
   35.6%; Score 38.5; I
40.0%; Pred. No. 24;
Live 3; Mismatches
                                                                                                                                                                                            || | : :|| | : || 648 GHSK-SRSKSSGDAQKSDDTACSQQ 671
                                                                                                                                               1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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Interpro; IPR003598; Ig_c2.
Interpro; IPR003609; Ig_like.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR001245; Tyr_pkinase.
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Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
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                                     Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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NCBI_TaxID=7227;
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(without alignments)
848.513 Million cell updates/sec
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                         108
1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                        671580 seqs, 206047115 residues
                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                     Title:
Perfect score:
                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                             Sequence:
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sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_bacteriap:* 1: sp_archea:* 2: sp_bacteria:* 3: sp_fungi:* sp_organelle:* sp_phage:* sp_archeap:* sp_plant:* sp_rodent:* sp_rvirus:* sp_mammal:* sp_mhc:* sp_human:* 10:

Maximum Match 100% Listing first 45 summaries

SPTREMBL 21:*

Database :

Post-processing: Minimum Match 0%

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ognim4 babesia mic Q9nim2 babesia mic Q24327 drosophila Q2433 drosophila Q9v643 drosophila O07532 bacillus su O9f855 vibrio chol Q91855 vibrio chol Q91856 vibrio chol Q91856 drosophila Q12288 saccharomyc Q9vby9 drosophila Q8viq4 mus musculu Q9vby9 drosophila Q8viq4 bomo sapien Q9nxa5 homo sapien Q9nxa5 homo sapien Q9nxa5 homo sapien Q9aer7 staphylococ Q40201 lotus japon Description Q9NIM4 Q9NIM2 Q24327 Q9V643 007532 Q9F855 Q9F855 Q8SZ45 Q12288 Q9VBY9 Q8VIQ4 Q9NXA5 Q9H945 Q9AER7 Q40201 16 Query Match Length DB 388 386 39.55 39.5 Score So. Result

O9NIM2 PRELIMINARY; PRT; 275 AA. O9NIM2; 01-OCT-2000 (TrEMBLrel. 15, Created) 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

RESULT 2 Q9NIM2

H A H H

Q99177 arabidopsis Q9bjz3 blastocrith O04503 arabidopsis Q84048 drosophila Q9vxw9 drosophila Q9vxw9 drosophila Q9net2 caenorhabdi Q9net2 caenorhabdi Q9net2 caenorhabdi Q9st190 thermotoga Q90cu9 human immun Q8487 dictyosteli Q2764 arabidopsis Q9189 arabidopsis Q91893 caenorhabdi Q9fm71 arabidopsis Q9fm71 arabidopsis Q9fm71 arabidopsis Q9fm71 arabidopsis Q9fm71 arabidopsis Q9fm70 caenorhabdi Q9fm30 clostridium Q9ffm8 neurospora Q9gp77 saccharomyc Q60949 mus musculu Q9fm30 clostridium Q9ffx1 bradythicob Q9fx1 bradythicob Q9fx1 bradythicob Q9fx1 homo sapien Q96b67 homo sapien	e) late) 1. Babesiidae, Babesia.	Mohamath R., Reynolds L.D., ing D.H.; immunoreactive antigens of EEGB7C CRC64; B 5; Length 396; s 14; Indels 0; Gaps 0; 32
61 10 09SL77 61 5 09Bu23 64 5 09Bu23 64 5 09Bu23 64 5 09WW9 84 5 09WW9 84 5 09WW9 82 5 02138 82 5 02138 82 5 021038 82 5 021038 82 5 021038 82 5 021038 82 5 021038 82 6 021038 82 6 021038 82 7 009Bu2 82 6 029Bu2 83 4 020Bu2 84 1 11 066949 86 16 09Bu2 86 16 09Bu2 87 10 09Pw3 87 10 09Pw3 88 10 09Fw3 89 10 09Fw3 80 10 0	ALIGNMENTS INARY; PRT; 396 AA. Strel. 15, Created) Strel. 15, Last sequence update) Strel. 15, Last annotation update) Hen BMN1-17 (Fragment). Ita; Apicomplexa; Piroplasmida; Ba	Hed S.G., Person and S.G., Person of novel (2000). Score 82; D Pred. No. 8. M. Mismatche (DTOTXQEXXXXXEE
17 35 32.4 261 19 35 32.4 361 20 35 32.4 462 21 35 32.4 122 22 34 31.5 368 23 34 31.5 368 24 31.5 368 368 25 34 31.5 368 26 34 31.5 492 27 34 31.5 492 28 34 31.5 492 30 34 31.5 408 31 34 31.5 1141 33 34 31.5 1141 36 34 31.5 1141 36 34 31.5 1141 36 34 31.5 1141 36 34 31.5 1141 36 34 31.5 1141 37 34 31.5 1141 38 30.6 32.7 41 33 30.6 33.6 42 33 30.6 33.6 43 30.6 414 30 6 414 31 30	1 9NIM4 PRELIMINA 1-OCT-2000 (TrEMBLE 1-OCT-2000	odes m. John Serologian Serologian D. Serologian m. Ject. I MBL; AF2 ON TER EQUENCE COUENCE LOCAL S. L
	RESULT 090 MAP 10 D 10 D 10 D 10 D 11 D 11 D 12 D 13 D 14 D 15 D 16 D 17 D 18 D 1	RA LA RA Ba RT Ba RT Ba RI DN EN SQ SI Matcl

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254 FYENDIVNDIKKNFDESKSKALVLRDKITKKDGDYNTHFEDMIKELNSAAEEFNKIVDIM 313
                                                              270 FSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLI 329
                                     210 LSAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIEN 269
                                                                                                                                                                                       330 ISDCEKKGIKINRDVISSYKLLLSTITYI-----VGAGVEAVTVSV 370
                                                                                                                                                                                                              ---SLMKKEELARIFDNAST--
   161 TKEKNKLKKELEKC-----FPEQY---
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
                                                                                 254 FYYDNIVNDIKKNFDESKSKALVLRDKITKKDGDYNTHFEDMIKELNSAAEEFNKIVDIM 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 PNTVGMSLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVK-----HDNYI--- 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    107 PNTVGMSLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVK------HDNYI--- 156
                                                                                                                              -----LKKEGEGCEQIYNYEEFIEKLRGARSEGNNMFQEALIR-FRNASSEEMVNAASY 209
                                                                                                                                                                                                                                -----LKKEGEGCEQIYNYEEFIEKLRGARSEGNNMFQEALIR-FRNASSEEMVNAASY 209
                                                                                                                                                                                                      210 LSAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIEN 269
                                                                                                                                                                                                                                                                                270 FSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLI 329
                     59; Gaps
                                                                                                                                                                   161 TKEKNKLKKELEKC-----FPEQY----SLMKKEELARIFDNAST----
                                                                                                                                                                                                                                                                                                                                                         330 ISDCEKKGIKINRDVISSYKLLLSTITYI------VGAGVEAVTVSV 370
                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 367;
                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPACTOR OPERATING SYSTEM: PC-DOS/MS-DOS COFFWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 COlumbia Center, 701 Fifth Avenue
 Pred. No. 1.2e-10;
; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . No. 1.2e-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%; Score 239.5; 29.3%; Pred. No. 1.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 20, Application US/08990571
Patent No. 6214971
Best Local Similarity 29.3%; Pr
Matches 85; Conservative 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (206) 622-4900
(206)682-6031
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CITY: Seattle
STATE: Washington
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
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US-08-990-571-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
US-08-990-571-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85;
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Best Local S
Matches 85
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                                                                                                                                                                                                                                         80 PADVAGVSD--GFFIRGONLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNEIYHTISSQI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       285 DGDYNTHFEDMIKELNSAAEEFNKIVDIMISNI---GDYDEYDSIASFKPFLSMITEITK 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYI-- 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 ---SLMKKEELARIFDNAST-----ISS---KYKLLVDEISNKAYGTLEGPAADNF 224
                                                                                                                                                                                                                                                                                                            Patent No. 61839, CGBNERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paull R.
TITLE OF INVENTION: COMPONINS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                           Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 4; Length 367;
                           DB 4;
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.30
                9.6%; Score 246.5; DB 4;
28.8%; Pred. No. 3.6e-11;
iive 53; Mismatches 113;
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-APR-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VGAGVEAVTVSV 370
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                      138 SNSFLIMMSDAIVK----
                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (206)682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Seattle
STATE: Washington
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OPERATING SYSTEM:
SOFTWARE: PAtentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                        Best_Local Similarity
Matches 92; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS
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                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---HDNYI-----LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 ---SLMKKEELARIFDNAST-----ISS---KYKLLVDEISNKAYGTLEGPAADNF 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
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Patent No. 6451315
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Reed, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Moughton, Raymond L.
APPLICANT: Moughton, Raymond L.
APPLICANT: Moughton, Raymond L.
APPLICANT: Moughton, Raymond L.
APPLICANT: MOUGH AND TREATHENT OF B. MICROIL INFECTION
TITLE OF INVENTION: AND TREATHENT OF B. MICROIL INFECTION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Local Similarity 28.8%; Pred. No. 3.6
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CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNE. (206) CETELEPHONE: (206) CETELEPK: (206)682-6031
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
CONTROL OF SEQUENCE CHARACTERISTICS
CONTROL OF
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STRANDEDNESS: sin
TOPOLOGY: linear
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LENGTH: 367
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Best Local 3
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241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80 PADVAGVSD--GFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNEIYHTISSQI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 PSEAGGPSEAGGPSGTGSEAGGWPSGTGWPSEAGWSSERF-GYQLLPYSRRI--VIFNEV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 SNSFLIMMSDAIVK------HDNYI------LKKEGEGCEQIYNYEEFIEKLRGAR 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Reed, Steven G.
APPLICANT: Reed, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9.6%; Score 246.5; DB 4;
28.8%; Pred. No. 3.6e-11;
tive 53; Mismatches 113;
                                                                                                                                                                                                                                           210121.426C2
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                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION:
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COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                        (206) 622-4900
(206) 682-6031
                                                                                                                     FILING DATE: 11-DEC-1997 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       : 367 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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MEDIUM TYPE: Floppy
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STATE: Washington
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Best Local Similarity
Matches: 92; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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US-08-990-571-49
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132 CLSYIYKHSVMILERDRVNDGHKDYIEEKTKEKNKLKKELEKC------FPEQY---- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               182 SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 PADVAGVSD--GFFIRGONLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNEIYHTISSQI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 PSEAGGPSEAGGPSGTGSEAGGWPSGTGWPSEAGWSSERF-GYOLLPYSRRI--VIFNEV 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138 SNSFLIMMSDAIVK------HDNYI------LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
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ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.6%; Score 246.5; DB 4;
28.8%; Pred. No. 3.6e-11;
tive 53; Mismatches 113;
                                                                                                                                                                     PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                   FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY, FAGENT IRRORMATION:
NAME: MALI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION:
                                                                                                                                                                                                               US/08/845,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 49, Application US/08990571 Patent No. 6214971 GENERAL INFORMATION:
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342 ITKVSNVIIPGIKALTLTV 360
                                                                                                                     IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID No: 49
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 28.00.
Thes 92; Conservative
                                                                                                                                                                  SOFTWARE: Patentin Rele
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
Washington
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                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acid
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COUNTRY: US
ZIP: 98104
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447 EGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                                                                      DLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGT
                                                                   387 GTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  334 EKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
APPLICANT: MCNeill, Patricia D.
APPLICANT: MCNEILON: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION CURRENT APPLICANTON NUMBER: US/09/528,784A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             METHODS FOR THE DIAGNOS: OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1143; DB 4;
Pred. No. 2.7e-79;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 90 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 49, Application US/08845258
Patent No. 6183976
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Applicant: Sloath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METATILE OF INVENTION: AND TREATMENT OF NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                US-09-528-784A-85; Sequence 85, Application US/09528784A; Patent No. 6451315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.68;
99.18;
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Best Local Similarity 99.1
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Babesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-528-784A-85
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                                                                                                                                                                                                                               DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
                                                                                                                                                                                                                                              DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------EFIEKLRGARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKE 219
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                                                                                    ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 DNI-----EDNNLKIYA-KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       369 IDFSKREATDSGSFTDILLGNKVKESLSFIEGLISDIKSHSLKAGVTGGISSSSLF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: MOMENII, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE REPERENCE: 210121.4266.4
CURRENT APPLICANTON NUMBER: US/99/528,784A
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58.3%; Pred. No. 3.2e-80;
11ve 35; Mismatches 89
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 87, Application US/09528784A
; Patent No. 6451315
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278; Conservative
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Matches 27
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US-08-723-142A-21
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US-09-528-784A-21
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                                                                                                                                                                                                                                                                     ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
                                                                                                                                                                                                                                                                                                 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                        DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGVEAVIVSVSATSNGTESGCAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419
                                                                                                                                                                                                                                                                                     1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIACNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                  Length 492;
                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                               Score 2130; DB 4;
Pred. No. 7.1e-155;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/723,142A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 21, Application US/08723142A Patent No. 6306396
                                                                                               83.0%;
             LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                             Conservative
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SEED AND STREET: 6300 Columb CITY: Seattle STATE: Washington
                                                         linear
                                                                                                              Similarity
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                                                         TOPOLOGY:
                                                                                               Query Match
Best Local Simi
Matches 417;
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                                                                     US-08-990-571-21
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APPLICANT Reed, Michael J.
APPLICANT Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Moneill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.4.26C4
CURRENT APPLICATION UNDBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEO ID NOS: 90
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Pred. No. 7.1e-155;
0; Mismatches 2;
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}; Pred. No. 7.1e-155;
. 0; Mismatches 2;
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99.5%;
TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        83.0%;
99.5%;
                                                                                  LENGTH: 492 amino acids TYPE: amino acid
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Best Local Similarity 99.5
Matches 417; Conservative
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Best Local Similarity 99.5
Matches 417; Conservative
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INFORMATION FOR SEQ ID NO:
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US-08-845-258-21
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        DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
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CURLICATION NOTA:
FILLING DATE: 24-APR-1997
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NAME: MAKI, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               ASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: SEED AND
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Washington
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Mashington
COUNTRY: USA
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                          83.0%; Score 2130; DB 4; 99.5%; Pred. No. 7.1e-155;
                                                                                                                                                                                                    0; Mismatches
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APPLICANT: Reed, Steven G. et
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
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TELECOMMUNICATION INFORMATION:
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(206) 682-6031
                                     LENGTH: 492 amino acids TYPE: amino acid STRANDEDNESS:
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Matches 417; Conservative
                    SEQUENCE CHARACTERISTICS
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                                                                                         Length 503;
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100.0%; Pred. No. 4.3e-188;
Live 0; Mismatches 0;
                                                                                         100.0%; Score 2565; DB 4; 100.0%; Pred. No. 4.3e-188;
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Patent No. 6451315
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Bleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TITLE OF INVENTION: AND TREATMENT OF B. MICRE; FILE OF INVENTION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
                                                                                                                       0; Mismatches
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NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 52
LENGTH: 503
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                                            ORGANISM: Babesia Microti
US-08-990-571-52
                                                                                         Query Match
Best Local Similarity 100.
Matches 503; Conservative
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Matches 503; Conserv
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              MOLECULE TYPE:
ORIGINAL SOURCE
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                                                                                                                                                                                                   AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG 420
                                                                                                                                                                                                                                                                                                                                                                                    TSGTTTSSGAASCKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGH 480
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                                                                          61 IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKN 120
                                                                                                                       ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
                                                                                                                                                                                                                                             DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
                                                                                                                                                                                                                                                                                                        DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG 360
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KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
              RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THI
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210121.426C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 52, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAXI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 503 amino acids
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STATE: Washing
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Appl Appl Appl Appl

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US-08-845-258-25 US-08-990-571-25 US-08-721-25 US-09-528-744A-25 US-09-528-744A-25 US-08-77-155-29 US-08-175-155-29 US-08-482-0858-64

Sequence Sequence Sequence

Appl Appl Appl

Sequence

Sequence

US-08-475-411A-31 US-08-478-029A-31 -09-444-791A-64 US-08-707-237A-54 US-08-806-029-10 US-08-477-509B-83

463 463 11177 11177 11177 11177 11177 11177 11177 11177 11059

US-08-175-155-48

Sequence

Sequence Sequence Sequence Sequence Sequence

Sequence

ALIGNMENTS

us-09-853-079-52.rai

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(without alignments)
323.107 Million cell updates/sec
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                                                                     July 16, 2003, 17:42:54 ; Search time 45.8044 Seconds
                                                                                                                                 1 KRFNEHIDMNGIHYYYIDGS.....AKIPGIMTLTLFALLTFIVN
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         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-08-990-571-21
US-08-921-142A-21
US-09-528-784A-21
US-09-528-784A-87
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US-08-990-571-49
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US-08-9528-784A-24
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US-08-9528-784A-24
US-08-9528-784A-24
US-08-9528-784A-24
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                                                                  APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: SLEATH, SCHOONDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 503;
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                                                                                                                                                                                                                                                                                                                                                     COUNTRY:

ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-ARR-1997
''ASSIFICATION: 435
                                                                                                                                                                                                                                                               :: SEED AND BERRY
6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 2565; DB 4;
100.0%; Pred. No. 4.3e-188;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 210121.426C1 TELECOMMUNICATION INFORMATION:
                Sequence 52, Application US/08845258 Patent No. 6183976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                           BERRY
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Best Local Similarity 100.
Matches 503; Conservative
                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                             ADDRESSEE: SEED AND
STREET: 6300 Columb
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM:
US-08-845-258-52
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Sequence Sequence Sequence

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US-08-477-509B-94 US-08-482-085B-94 US-09-444-791A-94

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194.5 194.5 194.5 192 192 192

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12;
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                                                                                                                                                                                                                                                         182 SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
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75 PSEAGGPSEAGGPSGTGSEAGGGPSEAGGGSERF-GYQLLPYSRI--VIFNEV 131
                                                                                                                                                                                                                                   138 SNSFLIMMSDAIVK------HDNYI-----LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                                                                  241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               285 DGDYNTHFEDMIKELNSAAEEFNKIVDIMISNI---GDYDEYDSIASFKPFLSMITEITK 341
                                                                                                                             61; Gaps
other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                      9.6%; Score 246.5; DB 19; Length 367; 28.8%; Pred. No. 1e-08; tive 53; Mismatches 113; Indels 61;
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342 ITKVSNVIIPGIKALTLTV 360
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Best Local Similarity 28.8%
Matches 92; Conservative
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   especially
              infection.
                                          Sednence
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                                                                                                                                                                                                                               126
                                                                                                                                                                                                                                                        453
                                                                                                                                                                                                                                                                    The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are
                                                                                                                                                                               99
coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                   NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC
                                                                                                                                                                   STLIGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK
                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                    Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                        AGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sleath PR, McNeill PD,
                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia microti antigenic epitope fusion protein BaF-5.
                                                                                                     DB 23;
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                                                                                                     Score 1143; DB 23
Pred. No. 8.9e-69;
                                                                                                                             2; Mismatches
                                                                                                                 Pred. No.
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2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
                                                                                                     44.68;
99.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000US-0569098
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                 Local Similarity .
hes 228; Conservative
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                                                                                                               Similarity
                                                                            666 AA;
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07-SEP-2000;
10-OCT-2000;
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276 TDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEK 335
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                                                                                                                                                                                                                                                                                                                                                                                                                         336 KGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAG
                                                                                                                                                                                                              Gaps
useful for enhancing immune response against B. microti. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                              ö
                                                                                                                                                   677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                       Length
                                                                                                                                                                                                                 Indels
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                                                                                                                                                                            1.2e-68;
                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR;
                                                                                                                                                                         100.0%; Preu. ...
                                                                                                                                                       44.5%; Score 1141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sleath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 94-95; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection and in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Babesia microti antigen sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW56301 standard; Protein; 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97EP-0117067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-0845258.
96US-0723142.
                                                                                                                                                                            Best Local Similarity 100.
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-195465/18.
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                                                                                                                                                                                                                                                                           ABB88975
                                                                       Sequence
                                                                                     Query Match
Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective
                                                                                                                                                                                                                                                                    EGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                        SMDDIIA----MFSN------PNMYLVKVAYLQAIEHIFLISTKYND----IFDYT
                                                                                              -----EFIEKLRGARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKE
                                                                                                                             FDDELFKKANDNFGRDDG-----YDFDYINTKK-----ELVILASVLDGLDLIMERL
                                                                                                                                      IENFSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALN
                                                                                                                                                                     DLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGT
                                                                                                                                                                                                     GTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSS
                                                                                                                                                                                                                                    SLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSD-AIVKHDNYILKKEGEGCEQIYNYE
                               DNI-----EDNNLKIYA-KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM
                                                                                                             IDFSKREATDSGSFTDILLGNKVKESLSFIEGLISDIKSHSLKAGVTGGISSSSLF
Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PD;
                                                                                                                                                                                                                                                                                                                                                                               parasite; tick-borne illness; antigen; disease prevention.
                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McNeill
23;
                .68
                                                                                                                                                                                                                                                                                                                                                                   B. microti MN-10/BMNI-17 fusion protein SEQ ID
Score 1159.5; DB
Pred. No. 1.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR,
                35; Mismatches
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17-MAR-2000; 2000US-0528784.
                                                                                                                                                                                                                                                                                                                    Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-APR-2000; 2000WO-US09136
                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 patient
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                                                                                                                                                                                                                                                                                                                   AAB30230 standard;
                                                                                                                                                                                                                                                                                                                                                                                    rodent
                                                                                                                                                                                                                                                                                                                                                                                           disease diagnosis;
        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lodes
                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200060090-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          treating or immunity in
Query Match
Best Local Simi
Matches 278;
                                                                                                                                                                                                                                                                                                                                                   12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                   Babesiosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                   AAB30230;
                                                                             327
                                                                                                              369
                                                                                                                             220
                                                                                                                                                             267
                                29
                                                              113
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                                                                                                                                                                                                                            387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SG,
                                                                                                                                                                                                                                                                                                                                                                                                           Babesia
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                          The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                   333
                                                                                                                                                                                                                                                                                                                                            393
                                                                                                                                                                                                                                                                                                                                                         453
                                                                                                                                                                                                                                                                                                   99
                                                                                                                                                                                                                                                                                      EKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSAT
                                                                                                                                                                                                                                                                                                                                                                                                                    STLTCNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK
                                                                                                                                                                                                                                                                   274 NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          χ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGTGTSCTTTSSCTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                Length
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          McNeill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BaF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 useful for diagnosing a conent of a composition
                                                                                                                                                                                                21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein
                                                                                                                                                                                              Score 1143; DB 21;
Pred. No. 8.9e-69;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Babesia microti antigens, useful for diagn microti infection, and as component of a componence response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesia microti antigenic epitope fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            999
7; Page 108-111; 118pp;
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2000US-0605724.
2000US-065688.
2000US-0685436.
2000US-0737178.
                                                                                                                                                                                                44.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                   Best Local Similarity 99.1
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-216691/27.
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                                                                                                                                                              999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-2000;
07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
26-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG,
Secrist H
                                                                                                                                                                                                                                                                                                                                               334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB88975;
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--YDFDYINTKK-----ELVILASVLDGLDLIMERL

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GTSVSATSTLTGNGCTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSS 446
                                                                                                                                                                                                         EGAGSDKAGTGTSGTTTSSGTGAGGAGSGCPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                             --DEIF----DELNLDQATIRTLVAPLDWPLISDKSLHPSLKMVV---VLPGFFIV----
                                                                      267 IENFSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALN
                                                                                  DLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGT
  FDDELFKKANDNFGRDDG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-216691/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                  microti
                                                                                                                                                                                                                                                                                                                                                                         Babesia microti.
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                                                                                                                                                                                                                                                                                                                                                                                           WO200185947-A2.
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07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-FEB-2001;
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13-DEC-2000;
                                                                                                                                                                                                                                                                                                            20-JUN-2002
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           369
                                                   425
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                                                                                                                                                       387
                                                                                                                                                                                              447
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                                                                                                                                                                                                                                                                                        Qγ
                     372
                                         360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMDDIIA----MFSN------PNMXLVKVAXLQAIEHIELISTKYND----IFDYT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419
                                                                                          New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
           DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN
                                        DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG
                                                   SLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSD-AIVKHDNYILKKEGEGCEQIYNYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 DNI-----EDNNLKIYA-KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75;
                                                                                                                                                                                                                B. microti MN-10/BMNI-17/BMNI-15 fusion protein SEQ ID NO:
                                                                                                                                                                                                                                  parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                               McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1159.5; DB Pred. No. 1.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                                              Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 7; Page 112-116; 118pp; English.
                                                                                                                                                    AAB30231 standard; Protein; 1132 AA
                                                                                                                                                                                                                                                                                                                                                                                                               Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45.2%;
                                                                                                                                                                                                                                                                                                                                       05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                                                                                                           05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       278; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-686939/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1132 AA;
                                                                                                                                                                                                                                    Babesiosis; rodent
                                                                                                                                                                                                                                                disease diagnosis;
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                                                                                                                                                                                             12-FEB-2001
                                                                                                                                                                                                                                                                                                                   12-OCT-2000
                                                                                                                                                                                                                                                                   Babesia sp.
                                                                                                                                                                                                                                                                              Synthetic.
                                       301
                                                          373
                                                                               361
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                                                                                                                                                                         AAB30231;
                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel Babesia microti antigens and coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homer
                                                                                                                                                                                                                                                      Protozoacide; vaccine; antigeh; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McNeill PD,
                                                                                                                                                                                            antigenic epitope fusion protein BaF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sleath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 35; Page 116-120; 195pp; English.
   AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Houghton RL,
ABB88976 standard; Protein; 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000US-0569098.
2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
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                                                                                                                              (first entry)
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73 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
   433 AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTWFG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IEDNNLKIYAKOFKSVVTTPADVAGVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to novel Babesia microti antigens and to coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
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                                                                                                                                                                                                    Protozoacide; vaccine; antigen; antigenic epitope; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 2130; DB 23;
Pred. No. 1.9e-135;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RL, Sleath PR,
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                                                                            ABB88937 standard; Protein; 492
                                                                                                                                                                      Babesia microti antigen BMNI-4.
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2000US-065688.
2000US-0685436.
2000US-0737178.
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99.5%;
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                                                                                                                                         (first entry)
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Best Local Similarity 99.5
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-216691/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           492 AA;
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                                                                                                                                                                                                                                                                WO200185947-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                     13-DEC-2000;
26-FEB-2001;
                                                                                                                                                                                                                                                                                                                           09-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                           27-JUN-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                         10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2000;
                                                                                                                                        20-JUN-2002
                                                                                                                                                                                                                                                                                              15-NOV-2001
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                                                                                                           ABB88937;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptides containing an antigenic portion of Babesia microti antityen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I EDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 492;
                                                                                                                                                                                                                                                                                                                                           PD;
                                                                                    parasite; tick-borne illness; antigen;
disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                         McNeill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 2130; DB 21;
Pred. No. 1.9e-135;
                                                                                                                                                                                                                                                                                                                                         Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 72-73; 118pp; English
                                                            microti BMNI-4 antigen SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                         RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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99.5%;
                                                                                                                                                                                                                                                              05-APR-1999; 99US-0286488.
17-MAR-2000; 2000US-0528784.
                                                                                                                                                                                                                                05-APR-2000; 2000WO-US09136
                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                         Lodes MJ,
                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-686939/67
N-PSDB; AAC65081.
                                                                                            rodent
                                                                                                           disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      492 AA;
                                                                                                                                      Babesia microti
                                                                                                                                                                    WO200060090-A1.
                                12-FEB-2001
                                                                                           Babesiosis;
                                                                                                                                                                                                   12-OCT-2000
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AAB30191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                        Reed SG,
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IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 313 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific immunogenic portions of Babesia microti. AAX88993 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAX24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEDYKINFREMVNEVTCANTKFEALNDL11SDCEKKGIKINRDV1SSYKLLLST1TY1VG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
 Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                      present invention describes isolated polypeptides comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 492;
                                                                                                                                                                                                                             Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.0%; Score 2130; DB 20; 99.5%; Pred. No. 1.9e-135;
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                                                                                                                                                                                                                               Persing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                 New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                           Example 1; Page 72-74; 126pp; English.
                                                                                                                                                                                                                             Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB30191 standard; Protein; 492
                                                                                                                            98WO-US26437.
                                                                                                                                                        97US-0990571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best_Local Similarity 99.5
Matches 417; Conservative
                                                                                                                                                                                                                            Houghton R,
                                                                                                                                                                                                   (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                     WPI; 1999-385612/32
              immunity; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    492 AA;
                                                                                                                                                                                                                                                                                    N-PSDB; AAX88998
                                                                                                                                                                                    CORI-) CORIXA
                                                                                                                            11-DEC-1998;
                                                                     WO9929869-A1
                                                                                                                                                        11-DEC-1997;
                                                                                                                                                                                                                             Bruinsma E,
                                                                                                17-JUN-1999
                                                                                                                                                                                                                                          Sleath PR;
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AAB30191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGVEAVIVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                          The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antiqen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using: (a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 492;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2130; DB 19;
Pred. No. 1.9e-135;
                                         Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                        infection and in protective vaccines
                                                                                                                                                                                    English
                                         Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babesia microti antigen BMNI-4.
                                                                                                                                                                                                                                                                                                                                                                                                                           83.0%;
99.5%;
                                                                                                                                                                              Claim 1; Page 49-51; 113pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 99.5 ses 417; Conservative
                                         Lodes MJ,
             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY24342 standard;
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                                                                                N-PSDB; AAV22734
                                         Houghton R,
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AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419

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Similarity
                                             452 AA;
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01-OCT-1996;
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Best Local
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                                                                                                      DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG
                                                                                                             AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG
                                                                                                                                     RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
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                                                                                                                                                                                                                                                                                                                                                                                                           Homer MJ
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                                                                                                                                                                                                                                                                                  vaccine; antigen; antigenic epitope; infection
                                                                                                                                                                                                                                                                                                                                                                                                           PD,
                                                                                                                                                                                                                                                                                                                                                                                                          McNeil1
                                                                                                                                                                                                                                                                                                                                                                                                           Sleath PR,
                                                                                                                                                                                                                                                                     Babesia microti antigen MN-10 variant.
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                                                                                                                                                                                  ASNAKIPGIMTLTLFALLTFIVN 503
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2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
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                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                              Babesia microti.
                                                                                                                                                                                                                                                                                                          WO200185947-A2
                                                                                                                                                                                                                                                                                  Protozoacide;
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07-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG 420
     their
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                           DB 23; Length 452;
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                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                     Score 2239.5; DB 2:
Pred. No. 7.3e-143;
0; Mismatches 4;
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                                                                                                                                                                                                                           87.3%;
89.0%;
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96US-0723142.
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                                                                                                                                                                                                                                                                           445; Conservative
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1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEYEHTELAKEHCKKEKCVNVDN 60
                                                   The present invention relates to novel Babesia microti antigens and the coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                421 TSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGH
                                       AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                             Protozoacide; vaccine; antigen; antigenic epitope; infection.
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                                                                                                                                                           AA.
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                                                                                                                                             481 ASNAKIPGIMTLTLFALLTFIVN
                                                                                                                                                                                                                                       ABB88961 standard; Protein; 503
                                                                                                                                                                                                                                                                                                                     Babesia microti antigen MN-10.
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2000US-0656688.
2000US-0685436.
2000US-0737178.
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10-OCT-2000;
13-DEC-2000;
26-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
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                                                                                                                                                         parasite; tick-borne illness; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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100.0%; Pred. No. 9.8e-165;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                    Sleath PR,
                                                                                                                                52.
                                                                                                                                                                       disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 14; Page 96-98; 118pp; English.
                                                                                                                              B. microti clone antigen SEQ ID NO:
                                                 AAB30216 standard; Protein; 503 AA.
                                                                                                                                                                                                                                                                                                                                                                      Houghton RL,
                                                                                                                                                                                                                                                                           05-APR-2000; 2000WO-US09136
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17-MAR-2000; 2000US-0528784
                                                                                                      (first entry)
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Best Local Similarity 100.
Matches 503; Conservative
                                                                                                                                                                                                                                                                                                                                                                   Reed SG, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-686939/67
                                                                                                                                                        Babesiosis; rodent
                                                                                                                                                                       disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         503 AA;
                                                                                                                                                                                                Babesia microti.
                                                                                                                                                                                                                       WO200060090-A1.
                                                                                                    12-FEB-2001
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                                                                          AAB30216;
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Homer MJ;

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Gaps

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microti.

Babesia

WO9929869-A1

17-JUN-1999

97US-0990571

11-DEC-1998; 11-DEC-1997;

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                                                                                                                                                                                                                                                                                                       Babesia microti antigen MN-10 complementary open reading frame protein.
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                                                                                                                                                                                                                                                                                                                                                                                        ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA
                                                                                                                                                                                                                                                                    Gaps
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                                                                    one antigenic portion of a Balesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection by detecting specific antibodies of probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                         100.0%; Score 2565; DB 19; Length 503; llarity 100.0%; Pred. No. 9.8e-165;. Conservative 0; Mismatches 0; Indels 0;
                                                           sequence is that of a polypeptide comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English
             Infection and in protective vaccines
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                                   Claim 1; Page 99-101; 113pp;
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Matches 503; Conserv
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                                                                                                                                                                        The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY24327 and these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
                                                                                                                                                                                                                                                                                                                                                                                      1 KRENEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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                                      Persing D,
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                        New isolated Babesia microti polypeptides
                                                                                                                                                  Example 1; Page 107-108; 126pp; English.
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              MAYO FOUNDATION
                                         Houghton
                                                                                WPI; 1999-385612/32.
N-PSDB; AAX90016.
 CORP
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es 503; Conserv
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CORIXA
                                         Bruinsma E,
                                                     Sleath PR;
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              (MAYO-)
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:36:24; Search time 140.806 Seconds (without alignments) 476.010 Million cell updates/sec Run on:

US-09-853-079-52
2565
1 KRFNEHTDMNGIHYYYIDGS.....AKIPGIMTLTLFALLTFIVN 503 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

908470

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Databa

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		nery	ore Match Length DB ID . Description	AAW56302	503 20	503 21 AAB30216	503 23	452 23 ABB89024	492 19 AAW56281	492 20 AAY24342	492 21 AAB30191	492 23 ABB88937	1132 21 AAB30231
a	æ	Query	Match L	100.0	100.0	100.0	100.0	87.3	83.0	83.0	83.0	83.0	45.2
			Score	2565	2565	2565	2565	2239.5	2130	2130	2130	2130	1159.5
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Babesia microti an B. microti MN-10/B Babesia microti an	Repetitive protein FCB-SLP protein fr SELPF amino acid s SELPF synthetic pr Amino acid sequenc 158P1D7 SSH nuclei Babesia microti BM Babesia microti an B. microti BM Babesia microti an B. microti BM Babesia microti an B.
ABBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBBB	AAB72727 AAB63997 AAW26351 AAW26351 AAW3527 AAW56290 AAY24346 AAB30195
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1159.5 11143 11143 11143 11144 11144 11144 11144 11144 11143 1143	1994.5 1982 1982 1982 1991 1911 1911
	338 338 444 444 5

ALIGNMENTS

RESU	RESULT 1
AAWS	AAW56302
Ω	AAW56302 standard; Protein; 503 AA.
XX	
AC	AAW56302;
XX	
DŢ	28-SEP-1998 (first entry)
XX	
DE	Babesia microti MN-10 antiqen sequence.
XX	
ΚW	antiqen; detection; diagnosis; vaccine; tick-borne disease;
ΚM	differentiation; Lyme disease; ehrlichiosis.
XX	
SO	Babesia microti.
XX	
PN	EP834567-A2.
XX	
PD	08-APR-1998.
XX	
PF	01-OCT-1997; 97EP-0117067.
XX	
PR	24-APR-1997; 97US-0845258.
PR	01-OCT-1996; 96US-0723142.
XX	
ΡA	(CORI-) CORIXA CORP.
XX	
БĪ	Houghton R, Lodes MJ, Reed SG, Sleath PR;

9 WPI; 1998-195465/18. N-PSDB; AAV22748. XXXXX

Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid,

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Sequence
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                                                                                                                                                                                                                                                                         The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                      Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                        New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                                                          (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B. microti MN-10/BMNI-17/BMNI-15 fusion protein SEQ ID NO: 87.
                                                                                                                                                    Sleath PR, McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                           Length
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100.0%; Pred. No. 1.2e-12;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                175 GKPNTNKSEKAERKSHDTQTTQEICE 200
                                                                                                                                                                                                                                                     Claim 35; Page 160-163; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                     1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                    Houghton RL,
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                                                             2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
                              09-MAY-2001; 2001WO-US15192
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17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 100.0
Matches 26; Conservative
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                                                                                                                                                    Lodes MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Reed SG, Lodes MJ,
                                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-686939/67
                                                                                                                                                                                                                                                                                                                                                    677 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200060090-A1.
                                                            27-JUN-2000;
07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
26-FEB-2001;
                                                     10-MAY-2000;
          15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12-OCT-2000.
                                                                                                                                                              Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesia sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB30231;
                                                                                                                                                    Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
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                               antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
New polypeptides containing an antigenic portion of Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 139; DB 21;
Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                  Example 7; Page 112-116; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         869 GKPNTNKSEKAERKSHDTQTTQEICE 894
                                                                                                                                                                                                                                                                                                                                                                                                   prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: July 16, 2003, 17:46:46 Job time: 8.27825 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
100.0%;
Best Local Similarity , 100.0%;
Matches 26; Conservative 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1132 AA;
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us-09-853-079-195.rag

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RESULT 13
ABB88975
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                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                     Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                       tick-borne illness; antigen;
                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McNeil1
                                                                                                                                                                                                                                                                                                                                                                        B. microti MN-10/BMNI-17 fusion protein SEQ ID NO: 85.
                                                                                                                     Score 139; DB 23;
Pred. No. 7.8e-13;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 139; DB 21;
Pred. No. 1.1e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sleath PR,
                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Page 108-111; 118pp; English.
                                                                                                                                                                                                218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                               1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                      disease diagnosis; disease prevention.
                                                                                                                                                                                                                                                                                  AAB30230 standard; Protein; 666 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Houghton RL,
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100.0%;
                                                                                                                   100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                       parasite;
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17-MAR-2000; 2000US-0528784
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                                                                                                                                                                                                                                                                                                                                                                                                       Babesiosis; rodent
                                                                                                                                    Similarity
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                                                                                         481 AA;
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                                                                                                                                                                                                                                                                                                                                            12-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                   Query Match
Best Local S
Matches 26
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                                                                                          Sequence
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AAB30230
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The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                    Protozoacide; vaccine; antigen; antigenic epitope; infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babesia microti antigenic epitope fusion protein BaF-5.
                                                                                                            Babesia microti antigenic epitope fusion protein BaF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 139; DB 23;
100.0%; Pred. No. 1.1e-12;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               403 GKPNTNKSEKAERKSHDTQTTQEICE 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 35; Page 113-115; 195pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB88989 standard; Protein; 677 AA.
666 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Houghton RL,
                                                                                                                                                                                                                                                                                                                                                              2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
ABB88975 standard; Protein;
                                                                                                                                                                                                                                                                                                          2001WO-US15192
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                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-216691/27
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nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           666 AA;
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                                                                                                                                                                                          Babesia microti.
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                                                                                                                                                                                                                                                                                                        09-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                  27-JUN-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                              10-MAY-2000;
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                                                                                                                                                                                                                                                                    15-NOV-2001
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Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence
                                      ABB88975;
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Matches
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Gaps

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Indels

403

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GKPNTNKSEKAERKSHDTQTTQEICE 26

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Conservative

Local Similarity

26;

Best Loc Matches

Homer MJ;

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The present invention relates to novel Babesia microti antigens and their
                                                                                                                                                                                                                                                                                              The present invention relates to novel Babesia microti antigens and the coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                      New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing immune response against B. microti infections \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                             McNeill PD,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 139; DB 23;
ilarity 100.0%; Pred. No. 7.1e-13;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babesia microti antigenic epitope fusion protein.
                                                               Sleath PR,
                                                                                                                                                                                                               immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                       Example 1; Page 92-93; 195pp; English.
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                                                             Houghton RL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB89025 standard; Protein; 481
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2000US-0656688.
2000US-0685436.
2000US-0737178.
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                                                               Lodes MJ,
                        (CORI-) CORIXA CORP
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                                                                                                                            WPI; 2002-216691/27
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les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200185947-A2.
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10-OCT-2000;
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26-FEB-2001;
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                                                                                   Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secrist H:
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                                                               Reed SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
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B. microti BMNI-17 antigen reverse complement SEQ ID NO: 38.
                                                                                                                                                                                                                                                                                                                                                                                    McNeill PD;
                                         parasite; tick-borne illness; antigen; disease prevention.
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Pred. No. 7.1e-13;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                 Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 86-87; 118pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesia microti antigen epitope #1.
                                                                                                                                                                                                                                                                                                                                                                                 Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB88952 standard; Protein; 445
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0
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Local Similarity 100.0%;
les 26; Conservative 0
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2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
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17-MAR-2000; 2000US-0528784
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                                                                                                                                                                                                                                                                                                                                                                               Lodes MJ,
                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-686939/67
                                         Babesiosis; rodent
disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 AA;
                                                                                                      Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200185947-A2.
                                                                                                                                              WO200060090-A1
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13-DEC-2000;
26-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                 Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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Matches

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RESULT

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Gaps

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Length 275;

Indels

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The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of infection and in protective vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia microti BMNI-17 complement antigen sequence.
                                                                                                                                                                                                          ch 100.0%; Score 139; DB 23; Similarity 100.0%; Pred. No. 4.1e-13; 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  1 GKPNTNKSEKAERKSHDTQTTQEICE 26
              Example 1; Page 103; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 77-79; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       AAW56298 standard; Protein; 445 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0845258.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97EP-0117067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-SEP-1998 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1998-195465/18.
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                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                           275 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesia microti.
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                                                                                                                                                                         Sequence
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Sleath PR;

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Babesia microti antigen BMNI-17 complementary open reading frame protein.
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                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                  Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
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 Length 445;
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                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 139; DB 20;
larity 100.0%; Pred. No. 7.1e-13;
Conservative 0; Mismatches 0;
Score 139; DB 19;
Pred. No. 7.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing D,
                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated Babesia microti polypeptides
                                                                182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                    1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 91-92; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB30207 standard; Protein; 445 AA.
                                                                                                                                              AAY24358 standard; Protein; 445 AA
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100.0%;
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                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton R,
                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                immunity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-385612/32.
N-PSDB; AAX90012.
Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 AA;
                                                                                                                                                                                                                                                                                           Babesia microti.
                                                                                                                                                                                                                                                                                                                    WO9929869-A1.
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                                                                                                                                                                                                                                                                                                                                                                      11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruinsma E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2001
                                                                                                                                                                                              16-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                       AAY24358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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Matches
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                                                                                                                    RESULT 8
                                                                                                                                   AAY24358
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AAY24365 standard; Protein; 275 AA.

AAY24365

(first entry)

16-SEP-1999

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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                      New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McNeill PD,
                                                                                                                                                              Sleath PR, McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 139; DB 21;
100.0%; Pred. No. 4.1e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 98; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABB88962 standard; Protein; 275 AA
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                                                                                                                                                              Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babesia microti antiqen BMNI-20.
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2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
05-APR-2000; 2000WO-US09136
                                           05-APR-1999; 99US-028648B.
17-MAR-2000; 2000US-0528784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                (CORI-) CORIXA CORP.
                                                                                                                                                              Lodes MJ,
                                                                                                                                                                                                         WPI; 2000-686939/67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2002-216691/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babesia microti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Secrist H;
                                                                                                                                                           Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB88962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seguence
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                                                                                                                                                      Babesia microti antigen BMNI-20 complementary open reading frame protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes isolated polypeptides comprising specific immunogenic portions of Babbesia microti. AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. They microti infections. They remove in the present sequence represents a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                    Babesia microti; antigen; immunogen; diagnosis; infection; vaccine; immunity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing D, Reed SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babesiosis; rodent parasite; tick-borne illness; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 139; DB 20;
100.0%; Pred. No. 4.1e-13;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Page 109-110; 126pp; English.
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Lodes MJ,

Houghton R,

Bruinsma E,

Sleath PR;

WPI; 1999-385612/32.

N-PSDB; AAX90017

(MAYO-) MAYO FOUNDATION

(CORI-) CORIXA CORP

98WO-US26437 97US-0990571

11-DEC-1998; 11-DEC-1997;

Babesia microti

WO9929869-A1

17-JUN-1999

26; Conservative

Matches

ð qq

Local Similarity

275 AA;

Sequence Query Match AAB30217 standard; Protein; 275

AAB3021

B. microti clone antigen SEQ ID NO: 53

12-FEB-2001 (first entry)

XX DXX XX

disease diagnosis; disease prevention.

a microti. -A1.

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Gaps

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Homer MJ;

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Gaps

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Indels

50;

Length

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The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoasays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides comprising Babesia microti antigens and their . immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) than have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                            antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 139; DB 19; Best Local Similarity 100.0%; Pred. No. 4.1e-13; Matches 26; Conservative 0; Mismatches 0;
             Score 139; DB 23;
Pred. No. 5.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sleath PR;
                                            Mismatches
                                                                                                                                                                                                                                                                                Babesia microti BMNI-20 antigen sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                           56
                                                                                                      26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 101-102; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection and in protective vaccines
                                                                                           1 GKPNTNKSEKAERKSHDTQTTQEICE
                                                                           1 GKPNTNKSEKAERKSHDTQTTQEICE
                                                                                                                                                                                      Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reed SG,
                                                                                                                                                                                     AAW56303 standard; Protein; 275
                                            ö
             100.08;
ilarity 100.08;
Conservative 0
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96US-0723142.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1998-195465/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
              Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAV22749.
                                                                                                                                                                                                                                                                                                                                                               Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-1997;
01-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Houghton R,
                                                                                                                                                                                                                                                 28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                                            EP834567-A2
                                                                                                                                                                                                                                                                                                                                                                                                                           08-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                    AAW56303;
                                                                                                                                                       RESULT 3
                                                                                                                                                                        AAW56303
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                                                                                                      The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homer MJ;
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention
              New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                 Length 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McNeill PD,
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                ch 100.0%; Score 139; DB 23; Similarity 100.0%; Pred. No. 2.8e-14; 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sleath PR,
                                                                                                                                                                                                                                                                                                                                1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                               1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Page 185; 195pp; English.
                                                                           Page 185; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesia microti antigen peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                         ABB89012 standard; Protein; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2000US-0656688.
2000US-0685436.
2000US-0737178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-2001; 2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-FEB-2001; 2001US-0794764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-216691/27.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                    26 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200185947-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-2000;
07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed SG, I
Secrist H;
                                                                                                                                                                                                                     Sednence
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                                                                           Claim 2;
                                                                                                                                                                                                                                                                                Matches
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Gaps

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Indels

Length 275;

Title: Perfect score: Sequence:

Run on:

Scoring table:

Searched:

Database

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ALIGNMENTS
            AAB30230
ABB88975
ABB88989
                                              AAB30231
ABB88976
ABB89019
ABB89015
                                                                                                                                                                               ABBB9020
AAY35210
ABB90561
AAE20304
AAE20288
AAY34934
AAY56856
                                                                                                                                                                                                                                                                              ABB89018
AAB56745
ABB68410
AAG27807
AAG27806
                                                                                              ABB89010
AAY24359
AAB30208
ABB88953
AAG75092
AAY68823
ABB97465
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ABP42747
AAB25692
                                                                                                                                                                                                                                                                                                                                                     ABB66823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB89013 standard; Peptide; 26 AA
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                                                                                               ABB89013;
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ABB89013
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476.010 Million cell updates/sec
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| SIDS2/gcddata/geneseq/geneseqp-emb1/AA1981.DAT:*
| SIDS2/gcddata/geneseq-emb1/AA1981.DAT:*
| SIDS2/gcddata/geneseq-geneseqp-emb1/AA1991.DAT:*
| SIDS2/gcddata/geneseq-geneseqp-emb1/AA1995.DAT:*
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          GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                             US-09-853-079-195
139
1 GKPNTNKSERAERKSHDTQTTQEICE 26
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                                                        OM protein - protein search, using sw model
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Human colon cancer Amino acid sequenc Novel human protei Babesia microti an Chlamydia pneumoni Novel human diagno Babesia microti an

Human prostate can Drosophila melanog Arabidopsis thalia Arabidopsis thalia Drosophila melanog Drosophila melanog Human secreted pro

Human polypeptide Human ovarian anti Human secreted pro Human channel-rela

Babesia microti an Babesia microti an Babesia microti an Babesia microti an B. microti BMNI-17 Babesia microti an

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Babesia microti

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT

			Description	Rabbaia mioroti an	Babesia microti an	Babesia microti BM	Babesia microti an	B. microti clone a	Babesia microti an	Babesia microti BM	Babesia microti an	B. microti BMNI-17	Babesia microti an
SUMMARIES			ΙD	ARR9013	ABB89012	AAW56303	AAY24365	AAB30217	ABB88962	AAW56298	AAY24358	AAB30207	ABB88952
	æ			23	23	13	20	21	23	19	20	21	23
		Query	Length	26	0 10	275	275	275	275	445	445	445	445
		Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
			Score	139	139	139	139	139	139	139	139	139	139
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WPI; 2002-216691/27

Homer MJ; Protozoacide; vaccine; antigen; antigenic epitope; infection. McNeill PD, Babesia microti antigen BMNI-17 peptide BMNI17-4 Sleath PR, Houghton RL, 2000US-0605724. 2000US-0656688. 2000US-0685436. 2000US-0737178. 2001US-0794764. 09-MAY-2001; 2001WO-US15192 20000s-0569098 Lodes MJ, (CORI-) CORIXA CORP Babesia microti. WO200185947-A2. 10-MAY-2000; 27 - JUN - 2000; 07-SEP-2000; 10-OCT-2000; 13-DEC-2000; 26-FEB-2001; 15-NOV-2001 Secrist H; Reed SG,